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OM protein - protein search, using sw model

Run on: October 1, 2003, 18:52:57 ; Search time 82 Seconds
(without alignments)
29.035 Million cell updates/sec

Title: US-09-426-011d-3

Perfect score: 90

Sequence: 1 RRRPRPPYLPAPPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Genesec 19Jun03.*
1: /SIDSI/gcgdata/genesec/genesecp-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/genesec/genesecp-emb1/AA1981.DAT.*
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22: /SIDSI/gcgdata/genesec/genesecp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/genesec/genesecp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/genesec/genesecp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	15	21 AAB26885	PR-39 derived angi
2	90	100.0	15	22 AAB84691	Amino acid sequenc
3	90	100.0	15	22 AAB97277	PR-39 derived pept
4	90	100.0	19	17 AAW01452	Leukocyte O2- prod
5	90	100.0	26	17 AAW01447	Leukocyte O3- prod
6	90	100.0	26	19 AAW75723	Proline/Arginine r
7	90	100.0	39	14 AAR30491	Antibacterial pept
8	90	100.0	39	17 AAW01446	Leukocyte O2- prod
9	90	100.0	33	17 AAR94446	Synducin peptide (

10	90	100.0	39	17 AAR99121	Magainin-derived a
11	90	100.0	39	19 AAW75722	Proline/Arginine r
12	90	100.0	39	21 AAB26888	PR-39 peptide used
13	90	100.0	39	22 AAB84690	Amino acid sequenc
14	90	100.0	39	22 AAB97280	PR-39 peptide. Un
15	90	100.0	42	23 AAB07714	Antimicrobial pept
16	90	100.0	44	22 AAB51194	E. coli AMP gene p
17	83	92.2	14	17 AAW01450	Leukocyte O2- prod
18	83	92.2	14	19 AAW75725	Proline/Arginine r
19	75	83.3	23	17 AAW01451	Bactenecin peptide
20	66	73.3	18	16 AAR79211	Proline/Arginine r
21	66	73.3	20	19 AAW75730	Bactenecin peptide
22	66	73.3	23	16 AAR79209	Bactenecin peptide
23	66	73.3	35	16 AAR79212	Cationic peptide B
24	66	73.3	59	19 AAW66400	Cationic peptide B
25	66	73.3	59	21 AAY91699	Cationic cancer - t
26	66	73.3	59	24 ABU59576	Antimicrobial pept
27	66	73.3	60	23 AAB07713	E. coli AMP gene B
28	66	73.3	62	22 AAB51197	PR-39 derived angi
29	64	71.1	11	21 AAB26886	Amino acid sequenc
30	64	71.1	11	22 AAB84692	PR-39 derived pept
31	64	71.1	11	22 AAB97278	Pig arg/pro rich p
32	64	71.1	11	24 AAB33050	Propionibacterium
33	63	70.0	91	22 AAW61229	RCMV Toledo strain
34	61	67.8	336	17 AAW05520	Human protease pRT
35	60	66.7	953	23 AAW74761	Amino acid sequenc
36	60	66.7	953	23 AAB26888	Human gene 307-enc
37	59	65.6	38	24 ABR01253	Human secreted pro
38	59	65.6	38	24 AAB99763	Human secreted pro
39	59	65.6	39	21 AAB44779	Synducin peptide {
40	59	65.6	59	17 AAR94448	Human liver peptid
41	56.5	62.8	74	22 AAB58034	Peptide #10125 enc
42	56.5	62.8	74	22 AAB42619	Human brain expres
43	56.5	62.8	74	22 AAB63510	Human bone marrow
44	56.5	62.8	74	22 AAW76344	Peptide #10470 enc
45	56.5	62.8	74	22 AAB36433	

ALIGNMENTS

RESULT 1

AAB26885

ID AAB26885 standard; peptide: 15 AA.

AC AAB26885;

XX 01-FEB-2001 (first entry)

DE PR-39 derived angiogenesis regulatory peptide 1.

XX Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;

KW myocardial ischaemia; proteasome.

XX Synthetic.

XX WO200057895-A1.

XX 05-OCT-2000.

XX 16-MAR-2000; 2000WO-US07050.

XX 26-MAR-1999; 99US-0276868.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Simons M, Gao Y;

XX WPI; 2000-628319/60.

PT Stimulating angiogenesis in situ, useful e.g. for treating anoxia and infarction, by administering a PR-39 oligopeptide that regulates enzymatic activity of proteasomes -

XX PS Claim 12; Page 40; 51pp; English.

CC This invention relates to a method for the stimulation of angiogenesis in

CC situ within a targeted collection of viable cells. The method comprises

CC introducing, into the cytoplasm, at least a member of the PR-39

CC oligopeptide collective, which interacts with cytoplasmic proteasomes.

CC Part of the proteolytic activity of the proteasomes is selectively

CC altered so as to stimulate angiogenesis. The method is used to induce

CC angiogenesis in tissue that has suffered anoxia or infarction,

CC e.g. myocardial infarction or chronic myocardial ischaemia, and also to

CC study the mechanisms that control angiogenesis. The present sequence

CC represents a PR-39 derived peptide which interacts with the proteasome

CC and can be used in the method of the invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 90; DB 21; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPP 15

DB 1 RRRPRPPYLPRPP 15

RESULT 2

ID AAB84691 standard; peptide; 15 AA.

XX AAB84691;

DT 17-SEP-2001 (first entry)

XX Amino acid sequence of a PR-39 derived peptide (residues 1-15).

DE PR-39; IkappaBalpha degradation; NFkappaB transcription factor;

KW myocardial infarction; chronic myocardial ischemia; heart disease;

KW anoxia.

XX Unidentified.

OS WO200147540-A1.

XX 05-JUL-2001.

XX 27-DEC-2000; 2000WO-US35293.

XX 29-DEC-1999; 99US-0474967.

FA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PI Simons M, Gao Y;

PI WPI; 2001-441690/47.

DR Selective inhibition of IkappaBalpha degradation within targeted viable

PT cell collection, involves interacting PR-39 oligopeptide with

PT IkappaBalpha and proteasomes, and altering proteolytic activity of

PT proteasomes -

XX Claim 11; Page 58; 69pp; English.

XX The present sequence represents a PR-39 derived peptide. It is used

CC for selective inhibition of IkappaBalpha degradation within a targeted

CC cell collection in-situ. The method is useful for selectively inhibiting

CC IkappaBalpha protein degradation in situ, decreasing the activity of

CC NFkappaB transcription factor and selective control of NFkappaB-dependent

CC gene expression in situ. The PR-39 derived peptides are useful in the

CC treatment of myocardial infarction, chronic myocardial ischemia of

CC heart disease and anoxia.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 90; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPP 15

DB 1 RRRPRPPYLPRPP 15

RESULT 3

ID AAB97277 standard; peptide; 15 AA.

XX AAB97277;

DT 09-AUG-2001 (first entry)

XX PR-39 derived peptide PR-15.

DE PR-39; cathelin; inflammation; wound healing; myocardial infarction;

KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;

KW anoxia; chronic myocardial ischaemia; heart tissue.

XX Unidentified.

OS WO200130368-A1.

XX 03-MAY-2001.

XX 06-OCT-2000; 2000WO-US27552.

XX 25-OCT-1999; 99US-0426011.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PA Simons M, Gao Y;

PI WPI; 2001-355179/37.

DR Stimulation of angiogenesis and inhibition of proteasome mediated

PT degradation in cells, by introduction of PR-39 oligopeptide or its

PT N-terminal fragments or their conjugates, for use in anoxia and

PT infarction conditions -

XX Claim 12; Page 42; 52pp; English.

XX Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39

CC is a member of the the cathelin family of proteins, mature PR-39 is 39

CC amino acids in length (see AAB97280), and has been shown to play a role

CC in several inflammatory events including wound healing and myocardial

CC infarction. The PR-39 derived family of oligopeptides cause selective

CC inhibition of proteasome mediated degeneration of peptides and

CC stimulation of angiogenesis after their intracellular introduction to a

CC target cell. PR-39 derived peptides are able to interact with at least

CC the alpha7 subunit of the proteasomes, and therefore alter the

CC proteolytic activity of proteasomes such that a selective increased

CC expression of specific proteins occurs. The invention includes methods

CC for the selective inhibition of proteasome mediated peptide degradation.

CC The method provides means for stimulating angiogenesis as required in

CC living tissues and organs which have suffered defects or have undergone

CC anoxia and/or infarction, myocardial infarction or chronic myocardial

CC ischaemia of heart tissue. Examples are the myocardium, skeletal or

CC smooth muscle, artery or vein, lung, brain, kidney, spleen, liver,

CC gastrointestinal or nerve tissues, limbs, and extremities. A particular

CC example is after myocardial infarction or ischaemia.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 90; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPP 15
 | | | | | | | | | |
 DB 1 RRRPRPPYLP RPP 15

RESULT 4

AAW01452
 ID AAW01452 standard; peptide; 19 AA.

AC AAW01452;

XX 18-JUN-1997 (first entry)

XX Leukocyte O2- production inhibitor peptide PR19.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

XX WO9632129-A1.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-US04674.

XX 10-APR-1995; 95US-0419066.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.

XX Inhibition of leukocyte superoxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39

XX Disclosure; Page 27; 45pp; English.

XX AAW01447-W01454 represent fragments of the proline-arginine rich
 CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
 CC isolated from porcine small intestine, and has also been identified in
 CC human and porcine neutrophils. PR39 kills bacteria by interfering with
 CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
 CC mesenchymal cells. Syndecans are important in wound repair, showing that
 CC PR39 can be used in wound repair, as well as in antibacterial agents.
 CC These sequences, and PR39, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting
 CC tissue damage at the wound site caused by excessive oxygen radicals
 CC produced by these leukocytes. They can also be used to develop products
 CC for treating inflammatory disease states.

XX Sequence 19 AA;

Query Match 100.0%; Score 90; DB 17; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.0003;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPP 15

DB 1 RRRPRPPYLP RPP 15

RESULT 5

AAW01447

ID AAW01447 standard; peptide; 26 AA.

XX AAW01447;

XX 18-JUN-1997 (first entry)

XX Leukocyte O2- production inhibitor peptide PR26.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

XX WO9632129-A1.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-US04674.

XX 10-APR-1995; 95US-0419066.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.

XX Inhibition of leukocyte superoxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39

XX Claim 3; Page 26; 45pp; English.

XX AAW01447-W01454 represent fragments of the proline-arginine rich
 CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
 CC isolated from porcine small intestine, and has also been identified in
 CC human and porcine neutrophils. PR39 kills bacteria by interfering with
 CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
 CC mesenchymal cells. Syndecans are important in wound repair, showing that
 CC PR39 can be used in wound repair, as well as in antibacterial agents.
 CC These sequences, and PR39, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting
 CC tissue damage at the wound site caused by excessive oxygen radicals
 CC produced by these leukocytes. They can also be used to develop products
 CC for treating inflammatory disease states.

XX Sequence 26 AA;

Query Match 100.0%; Score 90; DB 17; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPP 15

DB 1 RRRPRPPYLP RPP 15

RESULT 6

AAW75723

ID AAW75723 standard; peptide; 26 AA.

XX AAW75723;

XX 19-NOV-1998 (first entry)

XX Proline/Arginine rich peptide PR-26.

XX Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;

KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 XX coronary bypass; organ transplantation surgery.

OS Synthetic.

XX WO9835690-A1.

XX 20-AUG-1998.

XX 17-FEB-1998; 98WO-US03207.

XX 16-FEB-1998; 98US-0024975.

XX 18-FEB-1997; 97US-0802306.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Ross CR, Shi J;

XX WPI; 1998-495359/42.

XX Reduction of reperfusion injury in temporarily occluded blood
 XX vessels - by administration of a peptide which is rich in proline
 XX or arginine residues

XX Claim 3; Page 14-15; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 XX administration into a mammal's bloodstream reduce reperfusion injury
 XX (production of reactive oxygen species, neutrophil adherence to
 XX endothelium, and extravasation of neutrophils). These peptides have two
 XX requirements: they contain the consensus sequence PXXP, where P is a
 XX proline residue and X is any amino acid residue, which has been found to
 XX inhibit superoxide production, and secondly they have arginine residues
 XX adjacent to these motifs, required for effective inhibition. It was
 XX established by structural and function analysis that a peptide should
 XX ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 XX correlated with the increase of length of peptides. The effectiveness
 XX of these peptides was determined by investigating the production of the
 XX neutrophil superoxide anion, and also the inhibition of neutrophil
 XX chemotaxis. From this, it was found that all of the peptides inhibited
 XX NADPH oxidase to some extent. All of the peptides also inhibit
 XX neutrophil oxidase activity. PR-39 is believed, to be the most potent
 XX endogenous down regulator of NADPH oxidase yet discovered, and from the
 XX data produced, it can be suggested to be involved in eliminating or
 XX reducing the reperfusion injury induced adhesion and extraction of
 XX neutrophils. The peptides are also useful in connection with surgical
 XX procedures such as coronary bypass and organ transplantation surgery.

XX Sequence 26 AA;

Query Match 100.0%; Score 90; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RP RP 15
 |||||
 Db 1 RRRPRPPYLP RP RP 15

RESULT 7

AAAR30491

ID AAR30491 standard; peptide; 39 AA.

XX AC AAR30491;

XX 25-MAR-2003 (updated)

DT 12-MAY-1993 (first entry)

XX DE Antibacterial peptide.

XX Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;
 XX veterinary medicine; prophylactic.

OS Sus scrofa domestica.

XX WO9222578-A1.

XX 23-DEC-1992.

XX 10-JUN-1992; 92WO-SB00394.

XX 14-JUN-1991; 91SE-0001838.

XX (BOWA/) BOWAN H G.

XX (JOER/) JOERNVALL H.

XX (LEEJ/) LEE J.

XX (MUTT/) MUTT V.

XX Boman HG, Joernvall H, Lee J, Mutt V;

XX WPI; 1993-018080/02.

XX New anti-bacterial polypeptide - active against Gram negative

XX bacteria

XX Claim 1; Page 10; 15pp; English.

XX This peptide was isolated from the small intestine of a pig. The
 XX small intestine is an important endocrine organ and many it. This
 XX physiologically active peptides have been isolated from it. This
 XX peptide inhibits the growth of, and may kill, bacteria, pref. gram
 XX negative bacteria. This peptide or its functional derivatives may be
 XX used in human or veterinary medicine for therapeutic or prophylactic
 XX use.
 XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 39 AA;

Query Match 100.0%; Score 90; DB 14; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RP RP 15
 |||||

Db 1 RRRPRPPYLP RP RP 15

RESULT 8

AAW01446

ID AAW01446 standard; peptide; 39 AA.

XX AC AAW01446;

XX 18-JUN-1997 (first entry)

XX Leukocyte O2- production inhibitor peptide PR39.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 XX antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 XX DNA synthesis; protein synthesis; inhibitor; synecan expression;
 XX mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 XX tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

XX WO9632129-A1.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-US04574.

XX 10-APR-1995; 95US-0419066.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.
XX Inhibition of leukocyte superoxide anion prodn. and attraction of
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39
XX
XX Claim 2; Page 26; 45pp; English.
XX
XX This sequence represents the proline-arginine rich antimicrobial peptide
CC PR39. The PR39 sequence was first isolated from porcine small intestine,
CC and has also been identified in human and porcine neutrophils. PR39
CC kills bacteria by interfering with DNA and/or protein synthesis. PR39
CC also induces syndecan expression on mesenchymal cells. Syndecans are
CC important in wound repair, showing that PR39 can be used in wound repair,
CC as well as in antibacterial agents. This sequence, and the fragments of
CC it shown in AA01447-W01454, can be used in the method of the invention.
CC The method of the invention is for inhibiting leukocyte superoxide anion
CC (O2-) production. The method comprises administering to a leukocyte a
CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
CC production. The peptides can be used as medicaments for fighting
CC infection by attracting leukocytes to a wound site and restricting tissue
CC damage at the wound site caused by excessive oxygen radicals produced by
CC these leukocytes. They can also be used to develop products for treating
CC inflammatory disease states.
XX
XX Sequence 39 AA;
XX
XX Query Match 100.0%; Score 90; DB 17; Length 39;
XX Best Local Similarity 100.0%; Pred. No. 0.00055;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RRRPPPYLP RP RP 15
XX |||||
XX DB 1 RRRPPPYLP RP RP 15
XX
XX RESULT 9
XX AAR94446
XX ID AAR94446 standard; peptide; 39 AA.
XX
XX AC AAR94446;
XX
XX DT 05-NOV-1996 (first entry)
XX
XX DE Syndecan peptide (PR-39) induces syndecan expression.
XX
XX KW Syndecan; induction; expression; syndecan-1; syndecan-4; surface;
XX mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;
XX decubitus; ulcers; keloids; skin burns; ischemic tissues;
XX hypercoagulation states; prevention; tumour metastasis; restenosis;
XX inhibition; angiogenesis; proliferation; tumour metastasis; restenosis;
XX
XX OS Synthetic.
XX
XX XX WO9609322-A2.
XX PN 28-MAR-1996.
XX
XX PF 22-SEP-1995; 95WO-US12080.
XX
XX PR 22-SEP-1994; 94US-0310722.
XX
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX PI Bernfield M, Gallo RL;
XX
XX DR WPI; 1996-188401/19.
XX
XX Modulating mesenchymal interaction by administration of syndecan -
PT used in the treatment of wounds, tumours, restenosis, etc
XX
XX Claim 4; Page 26; 34pp; English.

CC The present peptide is a synducan, which induces the expression of
CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.
CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of
CC the peptide were found to be identical to the 36 N-terminal amino
CC acids of PR-39, a Pro and Arg rich antibacterial peptide previously
CC found in porcine intestine (W09222578). Synducins may be used in
CC the treatment of stasis and decubitus ulcers, keloids, skin burns,
CC ischemic tissues and hypercoagulation states, prevention of tumour
CC metastasis, restenosis inhibition and endothelial cell angiogenesis
CC and proliferation induction.
CC Human microvascular endothelial cells were assayed for syndecan-4
CC expression following exposure to 5 % wound fluid, dbcAMP (1 mM).
CC The present peptide (10 microm) or a blank, to give respective
CC cell surface syndecan-4 values (MOD/m in) of approx. 1.75, 1.70,
CC 1.80 and 0.95.
XX
XX Sequence 39 AA;
XX
XX Query Match 100.0%; Score 90; DB 17; Length 39;
XX Best Local Similarity 100.0%; Pred. No. 0.00055;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RRRPPPYLP RP RP 15
XX |||||
XX DB 1 RRRPPPYLP RP RP 15
XX
XX RESULT 10
XX AAR99121
XX ID AAR99121 standard; peptide; 39 AA.
XX
XX AC AAR99121;
XX
XX DT 28-OCT-1996 (first entry)
XX
XX DE Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
XX
XX KW STD; sexually transmitted disease; HIV; human immunodeficiency virus;
XX herpes simplex virus; HSV; Neisseria gonorrhoeae; Candida; Chlamydia;
XX magainin; antimicrobial; squalamine.
XX
XX OS Synthetic.
XX
XX XX Key Location/Qualifiers
XX FH Modified-site 39
XX FT /note= "amidated"
XX
XX XX WO9608270-A2.
XX PN 21-MAR-1996.
XX
XX PD 13-SEP-1995; 95WO-US11675.
XX
XX PR 13-SEP-1994; 94US-0305475.
XX
XX PA (MAGA-) MAGAININ PHARM INC.
XX
XX PI Bedi G, Jacob L, Williams T, Zasloff M;
XX
XX DR WPI; 1996-179725/18.
XX
XX Inhibiting sexually transmitted disease e.g. HIV or herpes simplex -
PT by administering magainin antimicrobial or squalamine cpd. to
PT inhibit transmission
XX
XX PS Example 1; Page 32; 60pp; English.
XX
XX AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may
CC be used to treat sexually transmitted diseases (STDs) caused by
CC Chlamydia, HIV, herpes simplex virus, Neisseria gonorrhoeae or
CC Candida infection. The peptides inhibit STDs by either killing the
CC infectious organism, impeding the infection mechanism or
CC interrupting the replication cycle of the organism. Squalamine (an

CC aminosterol host defence molecule of the dog fish shark *Squalus*
 CC acanthias) and pGLa (a frog antimicrobial peptide) analogues may
 CC also be useful in inhibiting STD infection and transmission.

XX Sequence 39 AA;

Query Match 100.0%; Score 90; DB 17; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRPP 15
 DB 1 RRRPRPPYLPRRPP 15

RESULT 11

AAW75722
 ID AAW75722 standard; peptide; 39 AA.

XX AAW75722;

DT 19-NOV-1998 (first entry)

DE Proline/Arginine rich peptide PR-39.

KW Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
 KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 KW coronary bypass; organ transplantation surgery.

XX Synthetic.

PN WO9835690-A1.

PD 20-AUG-1998.

XX 17-FEB-1998; 98WO-US03207.

PR 16-FEB-1998; 98US-0024975.

PR 18-FEB-1997; 97US-0802306.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

PA Blecha F, Ross CR, Shi J;

XX WPI; 1998-495359/42.

XX Reduction of reperfusion injury in temporarily occluded blood
 vessels... by administration of a peptide which is rich in proline
 or arginine residues

XX Claim 3; Page 14; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 administration into a mammal's bloodstream reduce reperfusion injury
 (production of reactive oxygen species, neutrophil adherence to
 endothelium, and extravasation of neutrophils). These peptides have two
 requirements: they contain the consensus sequence PXXP, where P is a
 proline residue and X is any amino acid residue, which has been found to
 inhibit superoxide production, and secondly they have arginine residues
 adjacent to these motifs, required for effective inhibition. It was
 established by structural and function analysis that a peptide should
 ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 correlated with the increase of length of peptides. The effectiveness
 of these peptides was determined by investigating the production of the
 neutrophil superoxide anion, and also the inhibition of neutrophil
 chemotaxis. From this, it was found that all of the peptides inhibited
 NADPH oxidase to some extent. All of the peptides also inhibit
 neutrophil oxidase activity. PR-39 is believed, to be the most potent
 endogenous down regulator of NADPH oxidase yet discovered, and from the
 data produced, it can be suggested to be involved in eliminating or
 reducing the reperfusion injury induced adhesion and extraction of
 neutrophils. The peptides are also useful in connection with surgical
 procedures such as coronary bypass and organ transplantation surgery.

XX Sequence 39 AA;

Query Match 100.0%; Score 90; DB 19; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRPP 15
 DB 1 RRRPRPPYLPRRPP 15

RESULT 12

AAW26888
 ID AAW26888 standard; peptide; 39 AA.

XX AAW26888;

DT 01-FEB-2001 (first entry)

DE PR-39 peptide used in angiogenesis control.

KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;
 KW myocardial ischaemia; proteasome.

XX Synthetic.

PN WO200057895-A1.

PD 05-OCT-2000.

XX 16-MAR-2000; 2000WO-US07050.

PR 26-MAR-1999; 99US-0276868.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Simons M, Gao Y;

XX WPI; 2000-628319/60.

XX Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
 infarction, by administering a PR-39 oligopeptide that regulates
 enzymatic activity of proteasomes

XX Disclosure; Page 21; 51pp; English.

XX This invention relates to a method for the stimulation of angiogenesis in
 situ within a targeted collection of viable cells. The method comprises
 introducing into the cytoplasm, at least 1 member of the PR-39
 oligopeptide collective, which interacts with cytoplasmic proteasomes.
 Part of the proteolytic activity of the proteasomes is selectively
 altered so as to stimulate angiogenesis. The method is used to induce
 angiogenesis in tissue that has suffered anoxia or infarction,
 e.g. myocardial infarction or chronic myocardial ischaemia, and also to
 study the mechanisms that control angiogenesis. The present sequence
 represents the PR-39 peptide from which peptide used in the method of
 the invention are derived.

XX Sequence 39 AA;

Query Match 100.0%; Score 90; DB 21; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRPP 15
 DB 1 RRRPRPPYLPRRPP 15

RESULT 13

AAW84690
 ID AAW84690 standard; protein; 39 AA.

Tue Jul 6 16:40:31 2004

XX AC AAB84690;
XX DT 17-SEP-2001 (first entry)
XX DE Amino acid sequence of a PR-39 protein.
XX KW PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
XX KW myocardial infarction; chronic myocardial ischemia; heart disease;
XX KW anoxia.
XX OS Unidentified.
XX PN WO200147540-A1.
XX PD 05-JUL-2001.
XX PF 27-DEC-2000; 2000WO-US35293.
XX PR 29-DEC-1999; 99US-0474967.
XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX PI Simons M, Gao Y;
XX DR WPI; 2001-441690/47.
XX CC Selective inhibition of IkappaBalpha degradation within targeted viable
XX CC cell collection, involves interacting PR-39 oligopeptide with
XX CC IkappaBalpha and proteasomes, and altering proteolytic activity of
XX CC proteasomes -
XX PS Disclosure; Page 30; 69pp; English.
XX CC The present sequence represents a PR-39 protein. The specification
XX CC describes PR-39 derived peptides, which are used for selective
XX CC inhibition of IkappaBalpha degradation within a targeted cell collection
XX CC in-situ. The method is useful for selectively inhibiting IkappaBalpha
XX CC protein degradation in situ, decreasing the activity of NFkappaB
XX CC transcription factor and selective control of NFkappaB-dependent gene
XX CC expression in situ. The PR-39 derived peptides are useful in the
XX CC treatment of myocardial infarction, chronic myocardial ischemia of
XX CC heart disease and anoxia.
XX SQ Sequence 39 AA;
Query Match 100.0%; Score 90; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. NO. 0.00055;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRPRPPVLP RPP 15
Db 1 RRRPRPPVLP RPP 15
RESULT 14
AAB97280
ID AAB97280 standard; peptide; 39 AA.
XX AC AAB97280;
XX DT 09-AUG-2001 (first entry)
XX DE PR-39 peptide.
XX KW PR-39; cathelin; inflammation; wound healing; myocardial infarction;
XX KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;
XX KW anoxia; chronic myocardial ischemia; heart tissue.
XX OS Unidentified.
XX PN WO200130368-A1.
XX PR

PD 03-MAY-2001.
XX PF 06-OCT-2000; 2000WO-US27552.
XX PR 25-OCT-1999; 99US-0426011.
XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX PI Simons M, Gao Y;
XX DR WPI; 2001-355179/37.
XX CC Stimulation of angiogenesis and inhibition of proteasome mediated
XX CC degradation in cells, by introduction of PR-39 oligopeptide or its
XX CC N-terminal fragments or their conjugates, for use in anoxia and
XX CC infarction conditions -
XX PS Disclosure; Page 21; 52pp; English.
XX CC Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39
XX CC is a member of the cathelin family of proteins, mature PR-39
XX CC represented by the present sequence is 39 amino acids in length, and has
XX CC been shown to play a role in several inflammatory events including wound
XX CC healing and myocardial infarction. The PR-39 derived family of
XX CC oligopeptides cause selective inhibition of proteasome mediated
XX CC degradation of peptides and stimulation of angiogenesis after their
XX CC intracellular introduction to a target cell. PR-39 derived peptides are
XX CC able to interact with at least the alpha7 subunit of the proteasomes, and
XX CC therefore alter the proteolytic activity of proteasomes such that a
XX CC selective increased expression of specific proteins occurs. The invention
XX CC includes methods for the selective inhibition of proteasome mediated
XX CC peptide degradation. The method provides means for stimulating
XX CC angiogenesis as required in living tissues and organs which have suffered
XX CC defects or have undergone anoxia and/or infarction, myocardial infarction
XX CC or chronic myocardial ischemia of heart tissue. Examples are the
XX CC myocardium, skeletal or smooth muscle, artery or vein, lung, brain,
XX CC kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and
XX CC extremities. A particular example is after myocardial infarction or
XX CC ischaemia.
XX SQ Sequence 39 AA;
Query Match 100.0%; Score 90; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. NO. 0.00055;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRPRPPVLP RPP 15
Db 1 RRRPRPPVLP RPP 15
RESULT 15
AAB07714
ID AAB07714 standard; peptide; 42 AA.
XX AC AAB07714;
XX DT 10-JUN-2002 (first entry)
XX DE Antimicrobial peptide PR-39 C-terminal fragment.
XX KW Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
XX KW antigen presenting cell; adjuvant; porcine; PR-39.
XX OS Sus sp.
XX PN WO200213857-A2.
XX PD 21-FEB-2002.
XX PF 17-AUG-2001; 2001WO-BP09529.
XX PR 17-AUG-2000; 2000AT-0001416.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMEH.
PA Fritz J, Mattner P, Zauner W, Buschle M, Egyed A;
XX WPI; 2002-269154/31.
XX
XX Vaccine for active immunization or for preparing an adjuvant for
PT enhancing an immune response to at least one antigen, comprises at
PT least one antigen and at least one cathelicidin derived antimicrobial
PT peptide -
XX
XX Disclosure; Fig 3; 65pp; English.
XX
XX The invention relates to a vaccine comprising at least one antigen and at
CC least one cathelicidin derived antimicrobial peptide or its derivative.
CC The vaccine is useful for active immunization, especially of humans or
CC animals without protection against the specific antigen. The cathelicidin
CC derived antimicrobial peptide is useful in the preparation of an adjuvant
CC for enhancing the immune response to at least one antigen, where the
CC adjuvant enhances the uptake of at least one antigen in antigen
CC presenting cells (APC), and the adjuvant is added to the vaccine.
CC Sequences ABB07708-15 represent C-terminal fragments of antimicrobial
CC peptides of the cathelicidin family.
XX
SQ Sequence 42 AA;
Query Match 100.0%; Score 90; DB 23; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLPFRPP 15
| | | | | | | | | | | | | | | |
Db 1 RRRPRPPYLPFRPP 15

Search completed: October 1, 2003, 19:03:11
Job time : 83 secs

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OM protein - protein search, using sw model

Run on: October 1, 2003, 19:01:53 ; Search time 29 Seconds
(without alignments)
21.885 Million cell updates/sec

Title: US-09-426-01ld-3

Perfect score: 90
Sequence: 1 RRRPRPPYLPRPP 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUT COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	26	2	US-08-419-066-2
2	90	100.0	26	3	US-09-024-975-2
3	90	100.0	39	1	US-08-162-052-1
4	90	100.0	39	1	US-08-310-722-1
5	90	100.0	39	2	US-08-419-066-1
6	90	100.0	39	2	US-08-728-333-1
7	90	100.0	39	3	US-09-024-975-1
8	90	100.0	39	5	PCT-US95-12080-1
9	83	92.2	14	3	US-09-024-975-4
10	66	73.3	20	3	US-09-024-975-9
11	66	73.3	59	4	US-09-030-619-163
12	61	67.8	336	1	US-08-414-926A-26
13	61	67.8	336	2	US-09-926-922-26
14	61	67.8	336	3	US-09-283-682-26
15	61	67.8	336	3	US-09-527-657-26
16	59	65.6	59	5	PCT-US95-12080-3
17	55	61.1	93	4	US-09-252-991A-29133
18	55	61.1	311	4	US-09-252-991A-22406
19	54.5	60.6	425	4	US-09-252-991A-19054
20	54	60.0	594	4	US-09-252-991A-32578
21	53	58.9	18	1	US-08-205-938A-23
22	53	58.9	18	1	US-08-205-938A-24
23	53	58.9	18	3	US-09-230-180-26
24	53	58.9	18	4	US-09-030-619-96
25	53	58.9	18	4	US-09-030-619-158
26	53	58.9	18	4	US-09-030-619-159
27	53	58.9	18	5	PCT-US95-02626-23

Sequence 24, Appl
Sequence 6408, Ap
Sequence 25, Appl
Sequence 160, App
Sequence 25, Appl
Sequence 26492, A
Sequence 41, Appl
Sequence 41, Appl
Sequence 3, Appl
Sequence 29050, A
Sequence 8, Appl
Sequence 21389, A
Sequence 5, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 17939, A

28 53 58.9 18 5 PCT-US95-02626-24
29 52.5 58.3 129 4 US-09-328-352-6408
30 52 57.8 18 1 US-08-205-938A-25
31 52 57.8 18 4 US-09-030-619-160
32 52 57.8 18 5 PCT-US95-02626-25
33 52 57.8 144 4 US-09-252-991A-26492
34 51.5 57.2 355 3 US-08-483-533-41
35 51.5 57.2 355 4 US-09-283-471A-41
36 51.5 57.2 355 5 PCT-US91-06532-3
37 51.5 57.2 381 4 US-09-252-991A-29050
38 51 56.7 16 1 US-08-205-938A-8
39 51 56.7 16 5 PCT-US95-02626-8
40 51 56.7 159 4 US-09-252-991A-21389
41 51 56.7 180 3 US-09-187-331-5
42 51 56.7 180 4 US-09-470-946-5
43 51 56.7 195 3 US-09-187-331-1
44 51 56.7 195 4 US-09-470-946-1
45 51 56.7 263 4 US-09-252-991A-17939

ALIGNMENTS

RESULT 1
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jieshu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSER: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match 100.0%; Score 90; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8e-05; 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLPRPP 15

Db 1 RRRPPPYLPRPP 15

RESULT 2

US-09-024-975-2
; Sequence 1, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-2

Query Match 100.0%; Score 90; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPYLPRPP 15
Db 1 RRRPPPYLPRPP 15

RESULT 3

US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5489575
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong-Youn
; APPLICANT: BOMAN, Hans G
; APPLICANT: MUTT, Viktor
; APPLICANT: JORNVAL, Hans
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,052
FILING DATE: 02-JUN-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9101838-2
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92-22578
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 0033000-299
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-162-052-1

Query Match 100.0%; Score 90; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPYLPRPP 15
Db 1 RRRPPPYLPRPP 15

RESULT 4

US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508


```

RESULT 7
US-09-024-975-1
; Sequence 1, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-024-975-1

Query Match 100.0%; Score 90; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRPP 15
DB 1 RRRPPPYLPRPP 15

RESULT 8
PCT-US95-12080-1
; Sequence 1, Application PC/TUS9512080
; GENERAL INFORMATION:
; APPLICANT: Children's Medical Center Corporation
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12080
; FILING DATE:
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-815-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Bonan, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jorvall, Hans
; TITLE: Novel Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
PCT-US95-12080-1

Query Match 100.0%; Score 90; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPRPP 15
DB 1 RRRPPPYLPRPP 15

RESULT 9
US-09-024-975-4
; Sequence 4, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-4

Query Match 92.2%; Score 83; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPLPRRP 14
DB 1 RRRPPPLPRRP 14

RESULT 10

US-09-024-975-9
Sequence 9, Application US/09024975
Patent No. 6133233

GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306

FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050

TELEFAX: 816/474-9057

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-024-975-9

Query Match 73.3%; Score 66; DB 3; Length 20;
Best Local Similarity 85.7%; Pred. No. 0.041;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRPPPLPRRP 14
DB 2 RIRPPPLPRRP 15

RESULT 11

US-09-030-619-163
Sequence 163, Application US/09030619B
Patent No. 6503881

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 66081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 163
LENGTH: 59
TYPE: PRT
ORGANISM: Bos taurus
US-09-030-619-163

Query Match 73.3%; Score 66; DB 4; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.11;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRPPPLPRRP 14
DB 2 RIRPPPLPRRP 15

RESULT 12

US-08-414-926A-26
Sequence 26, Application US/08414926A
Patent No. 5721354

GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94306-2155

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/414,926A

FILING DATE: March 31, 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Cserr, Luann

REGISTRATION NUMBER: 31,822

REFERENCE/DOCKET NUMBER: AVIR-011/COUS

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-494-7622

TELEFAX: 415-857-0663

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 336 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

IMMEDIATE SOURCE:

CLONE: tol.22

FEATURE:

NAME/KEY: Protein

LOCATION: 1..336

OTHER INFORMATION: /label= U1151

US-08-414-926A-26

Query Match 67.8%; Score 61; DB 1; Length 336;
Best Local Similarity 78.6%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRPDPYLP RP 15
DB 279 RRPDPYLP RP 292

RESULT 13

US-08-926-922-26
Sequence 26, Application US/08926922
Patent No. 5925751
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cserr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,922
FILING DATE: September 10, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tol.22
FEATURE:
NAME/KEY: Protein
LOCATION: 1.336
OTHER INFORMATION: /label= UL151

US-08-926-922-26

Query Match 67.8%; Score 61; DB 2; Length 336;
Best Local Similarity 78.6%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRPDPYLP RP 15
DB 279 RRPDPYLP RP 292

RESULT 14

US-09-253-682-26
Sequence 26, Application US/09253682
Patent No. 6040170
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An

TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cserr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,682
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/926,922
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tol.22
FEATURE:
NAME/KEY: Protein
LOCATION: 1.336
OTHER INFORMATION: /label= UL151

US-09-253-682-26

Query Match 67.8%; Score 61; DB 3; Length 336;
Best Local Similarity 78.6%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRPDPYLP RP 15
DB 279 RRPDPYLP RP 292

RESULT 15

US-09-527-657-26
Sequence 26, Application US/09527657
Patent No. 6291236
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An

TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:

ADDRESSEE: Luann Cserr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/09/527,657
: FILING DATE: 17-Mar-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/926,922
: FILING DATE: September 10, 1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Cseri, Luam
: REGISTRATION NUMBER: 31,822
: REFERENCE/DOCKET NUMBER: AVIR 11A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 510-834-1448
: TELEFAX: 510-839-7810
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 336 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: IMMEDIATE SOURCE:
: CLONE: tol.22
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..336
: OTHER INFORMATION: /label= UL151
: SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-527-657-26

Query Match      67.8%; Score 61; DB 3; Length 336;
Best Local Similarity 78.6%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 RRPRPPVLP RPRPP 15
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Db      279 RRPPIPLQ RPRPP 292

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Search completed: October 1, 2003, 19:06:44
 Job time : 29 secs

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OM protein - protein search, using sw model

Run on: October 1, 2003, 19:03:18 ; Search time 27 seconds
(without alignments)
87.896 Million cell updates/sec

Title: US-09-426-011d-3

Perfect score: 90

Sequence: 1 RRRPPVLPYLRPP 15

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Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	90	100.0	39	15	US-10-014-147-1
4	83	92.2	14	15	US-10-014-147-7
5	75	83.3	23	15	US-10-014-147-3
6	66	73.3	59	9	US-09-030-619-163
7	60	66.7	953	9	US-09-888-615-66
8	56.5	62.8	74	9	US-09-864-761-45555
9	55	61.1	45	9	US-09-864-761-49065
10	55	61.1	273	15	US-10-156-761-8265
11	54	60.0	250	15	US-10-103-806-517
12	53	58.9	18	9	US-09-030-619-96
13	53	58.9	18	9	US-09-030-619-158
14	53	58.9	18	9	US-09-030-619-159
15	53	58.9	18	12	US-10-229-368-1

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Sequence 160, Appl
Sequence 14520, A
Sequence 2, Appli
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Sequence 21, Appli
Sequence 35, Appli
Sequence 237, Appl
Sequence 2258, Ap
Sequence 320, App
Sequence 643, App
Sequence 320, App
Sequence 438, App
Sequence 97, Appl
Sequence 7617, Ap
Sequence 204, App

16 53 58.9 18 12 US-10-225-087-1
17 53 58.9 18 15 US-10-181-654-4
18 52 57.8 18 9 US-09-030-619-160
19 52 57.8 260 15 US-10-156-761-14520
20 52 57.8 354 14 US-10-004-717-2
21 52 57.8 354 14 US-10-004-717-58
22 51 56.7 180 10 US-09-997-701-5
23 51 56.7 195 10 US-09-997-701-1
24 51 56.7 235 15 US-10-153-668-59
25 50.5 56.1 304 15 US-10-156-761-13550
26 50.5 56.1 392 10 US-09-747-835A-55
27 50.5 56.1 393 15 US-10-243-035-2
28 50.5 56.1 419 9 US-09-828-035-2
29 50.5 56.1 419 12 US-10-345-680-44
30 50.5 56.1 419 12 US-10-146-733-29
31 50.5 56.1 1122 12 US-10-188-869-13
32 50.5 56.1 1145 12 US-10-188-869-20
33 50.5 56.1 1314 10 US-09-747-835A-29
34 50 55.6 18 15 US-10-181-654-21
35 50 55.6 18 15 US-10-181-654-35
36 50 55.6 99 9 US-09-864-761-43778
37 50 55.6 146 10 US-09-989-920-237
38 50 55.6 327 12 US-10-017-161-2258
39 50 55.6 449 9 US-09-764-870-320
40 50 55.6 449 9 US-09-764-853-643
41 50 55.6 449 15 US-10-125-540-320
42 50 55.6 449 15 US-10-103-313-438
43 49.5 55.0 129 11 US-09-975-719-97
44 49.5 55.0 156 15 US-10-156-761-7617
45 49 54.4 223 14 US-10-052-254-204

ALIGNMENTS

RESULT 1
US-10-014-147-4
; Sequence 4, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-014-147-4

Query Match 100.0%; Score 90; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLRPRPP 15
Db 1 RRRPRPPYLRPRPP 15

RESULT 2

US-10-014-147-2
; Sequence 2, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-014-147-2

Query Match 100.0%; Score 90; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLRPRPP 15
Db 1 RRRPRPPYLRPRPP 15

RESULT 3

US-10-014-147-1

; Sequence 1, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-147-1

Query Match 100.0%; Score 90; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLRPRPP 15
Db 1 RRRPRPPYLRPRPP 15

RESULT 4

US-10-014-147-7
; Sequence 7, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;;   APPLICATION NUMBER: US/10/014,147
;;   FILING DATE: 07-Dec-2001
;;   CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;;   APPLICATION NUMBER: US/08/930,777A
;;   FILING DATE: October 8, 1997
;;   APPLICATION NUMBER: PCT/US96/04674
;;   FILING DATE: April 10, 1996
;; ATTORNEY/AGENT INFORMATION:
;;   NAME: Collins, John M.
;;   REGISTRATION NUMBER: 26,262
;;   REFERENCE/DOCKET NUMBER: 23625-A
;; TELECOMMUNICATION INFORMATION:
;;   TELEPHONE: (816) 474-9050
;;   TELEFAX: (816) 474-9057
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;;   LENGTH: 14 amino acids
;;   TYPE: amino acid
;;   TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-014-147-7

Query Match          92.2%; Score 83; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPYLPRLPRPP 14
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Db 1 RRRPPYLPRLPRPP 14

RESULT 5
US-10-014-147-3
; Sequence 3, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
;;
```

```
;;
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;;   LENGTH: 23 amino acids
;;   TYPE: amino acid
;;   TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-014-147-3

Query Match          83.3%; Score 75; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PRPPYLPRLPRPP 15
   |||||
Db 1 PRPPYLPRLPRPP 12

RESULT 6
US-09-030-619-163
; Sequence 163, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-030-619-163

Query Match          73.3%; Score 66; DB 9; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.96;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRPPYLPRLPRPP 14
   |||||
Db 2 RRRPPYLPRLPRPP 15

RESULT 7
US-09-888-615-66
; Sequence 66, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHITE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHARIDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 953
;;
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OTHER INFORMATION: MAP TO AC005973.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.88
OTHER INFORMATION: EST_HUMAN HIT: A1358103.1, EVALUATE 4.60e+00
US-09-864-761-49065

Query Match 61.1%; Score 55; DB 9; Length 45;
Best Local Similarity 76.9%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP-RRPP 13
||| ||| |||

Db 19 RRRPRPPGPPRPQ 31

RESULT 10

US-10-156-761-8265

Sequence 8265, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

PRIOR FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 8265

LENGTH: 273

TYPE: PRT

ORGANISM: Streptomyces avermitilis

US-10-156-761-8265

Query Match 61.1%; Score 55; DB 15; Length 273;
Best Local Similarity 70.6%; Pred. No. 51;
Matches 12; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 RRRPRPPYLP-RRPP 15
||| ||| |||

Db 224 RRRPRPPGSRPRHP 240

RESULT 11

US-10-102-806-517

Sequence 517, Application US/10102806

Publication No. US20030054421A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: P4103P1C1

CURRENT APPLICATION NUMBER: US/10/102,806

PRIOR FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 846

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 517

LENGTH: 250

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE
LOCATION: (118)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (161)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (204)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-517

Query Match 60.0%; Score 54; DB 15; Length 250;
Best Local Similarity 71.4%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP-RRPP 14
||| ||| |||

Db 202 RRRPRPPAAPRRPP 215

RESULT 12

US-09-030-619-96

Sequence 96, Application US/09030619B

Patent No. US20020035061A1

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Erfile, Douglas

APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 96

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Cationic Peptide Analogue

US-09-030-619-96

Query Match 58.9%; Score 53; DB 9; Length 18;
Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLP-RRPP 15
||| ||| |||

Db 4 RPPYLP-RRPP 14

RESULT 13

US-09-030-619-158

Sequence 158, Application US/09030619B

Patent No. US20020035061A1

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Erfile, Douglas

APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25

; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Apis mellifera
US-09-030-619-158

Query Match 58.9%; Score 53; DB 9; Length 18;
Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPQPRPP 15
|||:|:|
Db 4 RPYVLPQPRPP 14

RESULT 14

US-09-030-619-159
; Sequence 159, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Apis mellifera
US-09-030-619-159

Query Match 58.9%; Score 53; DB 9; Length 18;
Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPQPRPP 15
|||:|:|
Db 4 RPYVLPQPRPP 14

RESULT 15

US-10-229-368-1
; Sequence 1, Application US/10229368
; Publication No. US20030148945A1
; GENERAL INFORMATION:
; APPLICANT: McNicol, Patricia J.
; APPLICANT: Pawlak, Sonia K.
; APPLICANT: Rubinchik, Evelina
; APPLICANT: Cameron, Dale
; APPLICANT: Guarna, Maria Marta
; TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 660081.418
; CURRENT APPLICATION NUMBER: US/10/229,368
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Indolicidin peptide analogs
US-10-229-368-1

Query Match 58.9%; Score 53; DB 12; Length 18;
Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPQPRPP 15
|||:|:|
Db 4 RPYVLPQPRPP 14

Search completed: October 1, 2003, 19:07:18
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2003, 19:00:33 ; Search time 39 Seconds
(without alignments)
36.988 Million cell updates/sec

Title: US-09-426-011d-3

Perfect score: 90

Sequence: 1 RRRPPPYLRRPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*

1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	172	2 S68232	antimicrobial prot
2	66	73.3	59	2 A36589	bactescin 7 - bov
3	59.5	66.1	82	2 A41051	spore coat protein
4	58	64.4	190	2 S68230	antimicrobial pept
5	56.5	62.8	168	2 S35330	apidaecin 14 precu
6	56.5	62.8	199	2 S14981	extensin class I (
7	55	61.1	437	2 A88942	protein R13D11.3 (
8	54.5	60.6	301	2 JQ1663	hybrid proline-ric
9	54	60.0	359	2 T13478	hypothetical prote
10	54	60.0	427	2 T32652	hypothetical prote
11	53	58.9	26	2 S06675	apidaecin 1b precu
12	53	58.9	144	2 S35331	apidaecin 22 precu
13	53	58.9	184	2 T29373	hypothetical prote
14	53	58.9	283	2 S35332	apidaecin 73 precu
15	53	58.9	428	2 E71415	probable coll wall
16	52	57.8	491	2 T07598	proline-rich prote
17	52	57.8	261	1 WMBEXE	infected cell prot
18	52	57.8	439	2 S51939	chitinase (EC 3.2.
19	52	57.8	467	2 S71169	protein kinase, 54
20	52	57.8	1006	2 G86292	hypothetical prote
21	51.5	57.2	1187	1 JC4155	protein-tyrosine-p
22	51.5	57.2	1189	1 JC2366	protein-tyrosine-p
23	51	56.7	180	2 S43791	PBX protein - hum
24	50.5	56.1	1216	2 JWO105	synaptotagmin 2 alp
25	50	55.6	192	2 S76867	hypothetical prote
26	50	55.6	383	2 T06753	zinc finger protei
27	50	55.6	415	1 S34170	acrosin (EC 3.4.21
28	50	55.6	421	1 S25599	acrosin (EC 3.4.21
29	50	55.6	424	2 A54964	spliceosome-associ

30	50	55.6	449	2 S16748	proline-rich prote
31	50	55.6	547	2 C96828	unknown protein F1
32	50	55.6	1460	1 EBBE1F	immediate-early pr
33	50	55.6	3036	2 T18995	hypothetical prote
34	49.5	55.0	589	2 T29299	hypothetical prote
35	49	54.4	118	2 T19345	hypothetical prote
36	49	54.4	134	2 JC5572	proline-rich prote
37	49	54.4	161	2 F72593	hypothetical prote
38	49	54.4	210	2 T33700	hypothetical prote
39	49	54.4	218	2 T22261	hypothetical prote
40	49	54.4	296	2 A27319	gliadin - wheat
41	49	54.4	296	2 S07361	alpha/beta-gliadin
42	49	54.4	352	2 F84799	hypothetical prote
43	49	54.4	369	2 S20500	hydroxyproline-ric
44	49	54.4	380	2 T32944	hypothetical prote
45	49	54.4	413	2 H87604	hypothetical prote

ALIGNMENTS

RESULT 1

S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N:Alternate names: myeloid antibacterial protein PR-39
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68232; JN0899; I47138; S19563
R:Zhao, C.; Ganz, T.; Lehrer, R.I.
F885 let. 376, 130-134, 1995
A:Title: Structure of genes for two cathelin-associated antimicrobial peptides: proph
A:Reference number: S68232; MUID:96105365; PMID:7498526
A:Accession: S68232
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-172 <ZHA>
A:Cross-references: EMBL:X89201; NID:gl165150; PIDN:CAA61487.1; PID:gl165151
A:Experimental source: leukocytes
R:Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A:Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to th
A:Reference number: JN0899; MUID:94071853; PMID:8250863
A:Accession: JN0899
A:Molecule type: mRNA
A:Residues: 1-20, 'A', 22-172 <STO>
A:Cross-references: GB:I23825; NID:9435100; PIDN:AAA31109.1; PID:9435101
A:Experimental source: bone marrow cells
R:Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; B
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A:Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene f
A:Reference number: I47138; MUID:95350216; PMID:7624374
A:Accession: I47138
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>
A:Cross-references: EMBL:X87236; NID:9829142; PIDN:CAAC0682.1; PID:gl051298
R:Agarberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernva
Eur. J. Biochem. 202, 845-854, 1991
A:Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of
A:Reference number: S19563; MUID:92111534; PMID:1765098
A:Accession: S19563
A:Molecule type: protein
A:Residues: 131-169 <AGE>
A:Experimental source: intestine
C:Genetics:
A:Gene: PR39
A:Introns: 66/3; 102/3; 126/3
C:Superfamily: cathelin; cystatin homology
C:Keywords: amidated carboxyl end; antibacterial
F:1-29/Domain: signal sequence #status predicted <SIG>
F:22-129/Domain: cystatin homology <Cys>
F:30-130/Domain: propeptide #status predicted <PRO>
F:131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

F:169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

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Query Match          100.0%; Score 90; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 0.00036;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 RRRPRPPYLPRRPP 15
 |||||
DB 131 RRRPRPPYLPRRPP 145

RESULT 2

AJ36589
bactenecin 7 - bovine
C:Species: Bos primigenius taurus (cattle)
C:CDate: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-May-1997
C:Accession: AJ36589
R:Frank, R.W.; Genmaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
J. Biol. Chem. 265, 18871-18874, 1990
A:Title: Amino acid sequences of two proline-rich bactericins. Antimicrobial peptides of
A:Reference number: AJ36589; MUID:91035404; PMID:2229048
A:Accession: AJ36589
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-59 <FRA>
C:Superfamily: cathelin; cystatin homology

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Query Match          73.3%; Score 66; DB 2; Length 59;  
Best Local Similarity 85.7%; Pred. No. 0.087;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 RRRPRPPYLPRRP 14
 |||||
DB 2 RIRPRPRLPRRP 15

RESULT 3

A41051
spore coat protein precursor - Bacillus subtilis
C:Species: Bacillus subtilis
C:CDate: 03-Apr-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2002
C:Accession: S04835; A41051; F69606
R:Aronson, A.I.; Song, H.Y.; Bourne, N.
Mol. Microbiol. 3, 437-444, 1989
A:Title: Gene structure and precursor processing of a novel Bacillus subtilis spore coat
A:Reference number: S04835; MUID:89313296; PMID:2546006
A:Accession: S04835
A:Molecule type: DNA
A:Residues: MNVTFNLSTRNWVGKIKAREVELL, 2-82 <AR2>
A:Cross-references: EMBL:X131740; NID:G39864; PIDN:CAA32004.1; PID:g39865
A:Experimental source: strain JH642
A>Note: part of this sequence, including the amino end of the mature protein, was confir
R:Bourne, N.; FitzJames, P.C.; Aronson, A.I.
J. Bacteriol. 173, 6618-6625, 1991
A:Title: Structural and germination defects of Bacillus subtilis spores with altered con
A:Reference number: A41051; MUID:92011439; PMID:1917883
A:Accession: A41051
A:Molecule type: protein
A:Residues: 'XX', 3-11 <BOU>
A:Experimental source: strain JH642
A>Note: the material sequenced was the larger of two isolated precursor forms, the amino
R:Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, M.M.; Chd
A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Puma, S.; Galizzi, A.; Gallen
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.P.
Koetter, P.; Koningsstegen, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinou
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
Y. M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
tbaer, M.; Schleib, S.; Schuster, P.; Scoffone, P.; Sekowska, A.; Seron
tbaer, M.; Schleib, S.; Schuster, P.; Scoffone, P.; Sekowska, A.; Seron

Kunita, K.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, Y.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis* strain 168
 Reference number: A69580; MUID:98044033; PMID:9384377
 Accession: F6906
 Status: preliminary; nucleic acid sequence not shown; translation not shown
 Molecule type: DNA
 Residues: 110
 Cross-references: GB:299110; GB:AL009126; NID:G2633472; PIDN:CAB13066.1; PID:G263353
 Experimental source: strain 168
 Comment: This structural protein is expressed during stage V of sporulation.
 C:Genetics:

Query Match 66.1%; Score 59.5; DB 2; Length 82;
 Best Local Similarity 84.6%; Pred. No. 0.7; Indels 1; Gaps 1;
 Matches 11; Conservative 0; Mismatches 0

QY 4 PRPP-YLPRPRPP 15
 DDB 49 PRPPYVPRPP 61
 ||||| |||||
 ||||| |||||

RESULT 4
 GS68230
 antimicrobial peptide precursor - sheep
 Alternate names: Bac7.5 peptide homolog
 Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S68230
 R:Bagella, L.; Scocchi, M.; Zanetti, M.
 FEBS Lett. 376, 225-228, 1995
 A:Title: cDNA sequences of three sheep myeloid cathelicidins.
 A:Reference number: S68228; MUID:96105386; PMID:7498547
 A:Accession: S68230
 Status: preliminary
 Molecule type: mRNA
 Residues: 1-190 <BAG>
 Cross-references: EMBL:L46852; NID:G1161244; PIDN:AAA85468.1; PID:G1161245
 Superfamily: cathelin; cystatin homolog
 P:1-29/Domain: signal sequence #status predicted <SIG>
 F:22-129/Domain: cystatin homolog <YS>
 F:29-130/Domain: propeptide #status predicted <PRO>
 P:130-190/Product: antimicrobial peptide #status predicted <MAT>

Query Match 64.4%; Score 58; DB 2; Length 190;
 Best Local Similarity 78.6%; Pred. No. 2.4;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPP 14
 DDB 132 RLRRPRRLPRPP 145
 ||||| |||||
 ||||| |||||

RESULT 5
 S35330
 apidaecin 14 precursor - honeybee
 Contains: apidaecin II
 Species: Apis mellifera (honeybee)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C:Accession: S35330; S06676
 R:Casteele-Josson, K.; Capaci, T.; Casteele, P.; Tempst, P.
 EMBO J. 12, 1569-1578, 1993
 A:Title: Apidaecin multipetide precursor structure: a putative mechanism for amplification
 A:Reference number: S35330; MUID:93223697; PMID:8467807
 Accession: S35330
 Molecule type: mRNA
 Residues: 1-168 <CAS>

A:Cross-references: EMBL:X72575; NID:g297062; PIDN:CAA51167.1; PID:g297063
R:Casteels, P.; Ampe, C.; Jacobs, F.; Vaeck, M.; Tempst, P.
EMBO J. 8, 2387-2391, 1989
A:Title: Apidaecins: antibacterial peptides from honeybees.
A:Reference number: S05383; MUID:90005446; PMID:2674519

A:Accession: S06676
A:Molecule type: protein
A:Residues: 43-60 <Caz>
C:Superfamily: procyclic acidic repetitive protein
E:43-60/Product: apidaecin II #status experimental <MAT>

Query Match 62.8%; Score 56.5; DB 2; Length 168;
Best Local Similarity 50.0%; Pred. No. 3.2;
Matches 11; Conservative 2; Mismatches 2; Indels 7; Gaps 17

Qy 1 RRRP-----RPPYLRPP 15
||| ||| : : |||
db 117 RREPEAGNNRPVYIOPRPP 138

6. T. H. S. 6

extensin class I (clone w1-8 L) - tomato (fragment)
 S14981
 C:Species: Lycopersicon esculentum (tomato)
 C:SpecDate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
 C:Accession: S14981
 R:R.Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
 Plant Mol. Biol. 16, 547-565, 1991
 A:Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to wounding
 A:Reference number: S14970; MIMD:91329690; EMD:1714316

A;Accession: S14581
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-199 <SHO>

Accession: 130000
A; Cross-references: EMBL:X55692
A; Experimental source: cv. UC82B
C; Superfamily: hydroxyproline-ri-

C;Keywords: cell wall; glycoprotein; hydroxyproline

Query Match	62.8%	Score 56.5;	DB 2;	Length 199;
Best Local Similarity	73.3%	Pred. No. 3.8;		
Matches 11;	Conservative	0;	Mismatches	1;
			Indels	

Qy 4 PRPP---YIPPRPP 15
db 77 PRPPPPPPYIPPRPP 91

RESULTS

A88942
 protein R13D11.3 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: A88942
 R:anonymous. The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes
A:Reference number: A75000; PMID:9069613; PMID:9851916
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 282, 2012-2018, 1998
A:Accession: A88942
A:Status: preliminary

A:Molecule_type: DNA
A:Accessions: 1-437 <STO>
A:Cross-references: GB:chr_V; PIDN:AAB69949.1; PID:G2384928; GSFDB:GN000023; CESP:R13D11.1
C:Genetics:
A:Gene: R13D11.3
A:Map position: 5

Query Match 61.1%; Score 55; DB 2; Length 437;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 9: Conservative 1: Mismatches 2: Indels

Qy	4	PRPPYLPRPP	15
		:	
D _b	23	PRPPHPPIPRP	34

RESIT.T &

JQ1663
 hybrid proline-rich protein - maize
 C:Species: Zea mays (maize)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
 C:Accession: JQ1663
 R:Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.
 Plant Cell 4, 413-423, 1992
 A:Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein.
 A:Reference number: JQ1663; MUID:92361259; PMID:1498500
 A:Accession: JQ1663
 A:Molecule type: DNA
 A:Residues: 1-301 <JOS>
 A:Cross-references: EMBL:X60432; NID:g333706; PIDN:CAA42959.1; PID:g433707
 A:Experimental source: strain W64A
 C:Superfamily: hydroxyproline-rich glycoprotein

Query Match	60.6%;	Score 54.5;	DB 2;	Length 301;
Best Local Similarity	71.4%;	Pred. No. 9.7;		
Matches 10:	Conservative	1:	Mismatches	2:
			Indels	1:
			Gaps	1:

Qy 3 RPRPPYL-PRRPP 15
|||: |||
Db 149 RPSPPYVPTPRPP 16

DEC 11 1964

T13478
 hypothetical protein 34F3.10 - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
 C:Accession: T13478
 R:Valentini, P.; Salles, C.; Campbell, L.; Glover, D.
 submitted to the EMBL Data Library, April 1999
 A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
 A:Reference number: Z17685
 A:Accession: T13478
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <PHI>
 A:Cross-References: EMBL:AL031583; NID:e1321005; PID:e1321018; PIDN:CAB41346;
 C:Genetics:
 A:Cross-References: FlyBase:FBgm0025623
 A:Translation: 17/02/2002

Query Match	60.0%	Score 54;	DB 2;	Length 359;
Best Local Similarity	71.4%;	Pred. NO. 13;		
Matches 10:	Conservative	0:	Mismatches	4:
			Indels	0:
			Gaps	0:

Qy 2 RRRPPYLRPPPP 15
||| ||| ||| |||
pb 167 RRRPPPLPPPPPP 18

Page 10

hypothetical protein F39C12.3 - Caenorhabditis elegans
 T32652
 CSpecies: Caenorhabditis elegans
 CDate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 CAccession: T32652
 R.Chisoso, S.; Sansone, J.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid F39C12.
 A:Reference number: Z21206
 A:Accession: T32652
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule_type: DNA

A;Residues: 1-427 <CHI>
A;Cross-references: EMBL:AF039043; PIDN:AAE94196.1; GSPDB:GN00028; CESP:F39C12.3
A;Experimental source: strain Bristol N2; clone F39C12
C;Genetics:
A;Gene: CESP:F39C12.3
A;Map position: X
A;Introns: 42/3; 104/3; 133/3; 164/3; 213/3; 276/3; 336/3

Query Match 60.0%; Score 54; DB 2; Length 427;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RPPYLPRLPRPP 15
||| |
DB 338 RPPDPDIPPLPP 350
||| |

RESULT 11
S06675
apidaecin 1b precursor - honeybee
C;Species: Apis mellifera (honeybee)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Dec-1998
R;Casteels-Josson, P.; Ampe, C.; Jacobs, P.; Vaack, M.; Tempst, P.
EMBO J. 8, 2387-2391, 1989
A;Title: Apidaecins: antibacterial peptides from honeybees.
A;Reference number: S05383; MUID:90005446; PMID:2676519
A;Accession: S06675
A;Molecule type: protein
A;Residues: 1-26 <CAS>
F;1-8/Domain: propeptide #status experimental <PRO>
F;9-26/Product: apidaecin 1b #status experimental <MAT>

Query Match 58.9%; Score 53; DB 2; Length 26;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPRLPRPP 15
||| |
DB 12 RPVIQPRPP 22
||| |

RESULT 12
S35331
apidaecin 22 precursor - honeybee
C;Species: Apis mellifera (honeybee)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
R;Casteels-Josson, P.; Capaci, T.; Casteels, P.; Tempst, P.
EMBO J. 12, 1569-1578, 1993
A;Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplification
A;Reference number: S35330; MUID:93223697; PMID:8467807
A;Accession: S35331
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <CAS>
A;Cross-references: EMBL:X72576; NID:9297064; PIDN:CAA51168.1; PID:9297065
C;Superfamily: procyclic acidic repetitive protein

Query Match 58.9%; Score 53; DB 2; Length 144;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPRLPRPP 15
||| |
DB 46 RPVIQPRPP 56
||| |

RESULT 13
T29373
hypothetical protein ZC404.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

C;Accession: T29373
R;Bentley, D.; Le, T.T.
Submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid ZC404.
A;Reference number: Z20614
A;Accession: T29373
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-184 <BEN>
A;Cross-references: EMBL:U55363; PIDN:AAA97967.1; GSPDB:GN00023; CESP:ZC404.1
A;Experimental source: strain Bristol N2; clone ZC404
C;Genetics:
A;Gene: CESP:ZC404.1
A;Map position: 5
A;Introns: 15/2; 50/2; 75/2; 138/2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC404.1

Query Match 58.9%; Score 53; DB 2; Length 184;
Best Local Similarity 90.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RPPYLPRLPRPP 12
||| |
DB 26 RPPYLPRLPRPP 35
||| |

RESULT 14
S35332
apidaecin 73 precursor - honeybee (fragment)
N;Contains: apidaecin 1a
C;Species: Apis mellifera (honeybee)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Nov-2000
R;Casteels-Josson, P.; Capaci, T.; Casteels, P.; Tempst, P.
EMBO J. 12, 1569-1578, 1993
A;Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplification
A;Reference number: S35330; MUID:93223697; PMID:8467807
A;Accession: S35332
A;Molecule type: mRNA
A;Residues: 1-283 <CAS>
A;Cross-references: EMBL:X72577; NID:9297066; PIDN:CAA51169.1; PID:94539289
A;Accession: S05383
A;Molecule type: protein
A;Residues: 258-283 <CA3>
C;Superfamily: proline-rich protein
F;266-283/Product: apidaecin 1a #status experimental <MAT>

Query Match 58.9%; Score 53; DB 2; Length 283;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPRLPRPP 15
||| |
DB 45 RPVIQPRPP 55
||| |

RESULT 15
E71415
probable coll wall protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: Columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzensagger, T.; Pohl, T.M.; Terry, N.; G.avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, A.; Moeres, T.; Jones, J.D.G.; Eneva, T.; Palmer, K.; Benes, V.; Rechman, S.; C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: E71415

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-428 <BEV>
 A;Cross-references: GB:297338; NID:g2244870; PID:e327461; PID:g2244874
 C;Genetics:
 A;Map position: 4COP9-4G3845

Query Match 58.9%; Score 53; DB 2; Length 428;
 Best Local Similarity 61.5%; Pred. NO. 21;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRPYPYLRPRPP 15
 : |||||:
 Db 67 KPPPYIPCPPPP 79

Search completed: October 1, 2003, 19:06:09
 Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2003, 18:53:22 ; Search time 22 Seconds
(without alignments)
32.064 Million cell updates/sec

Title: US-09-426-011D-3
Perfect score: 90
Sequence: 1 RRRPRPPYLRPRPP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	90	100.0	172	1 PR39_PIG	P80054 sus scrofa
2	66	73.3	190	1 BCT7_BOVIN	P19661 bos taurus
3	59.5	66.1	107	1 COTT_BACSU	P11863 bacillus su
4	58	64.4	190	1 BCT7_SHEEP	P50415 ovis aries
5	56.5	62.8	168	1 AP14_APIME	Q06601 apis mellif
6	55.5	61.7	151	1 RNB_HSV2H	P89479 herpes simp
7	54	60.0	955	1 T150_HUMAN	Q9V2w1 homo sapien
8	53	58.9	144	1 AP22_APIME	P35581 apis mellif
9	53	58.9	283	1 AP73_APIME	Q06602 apis mellif
10	53	58.9	361	1 PRLP_BOVIN	Q9gkx8 bos taurus
11	52	57.8	261	1 RLI_HSV2H	P28283 herpes simp
12	52	57.8	354	1 AFCH_HUMAN	Q92858 homo sapien
13	52	57.8	467	1 AFCH_ARATH	P51566 arabidopsis
14	52	57.8	841	1 RELA_STEAT	O85709 streptomyce
15	51.5	57.2	1187	1 PTNE_HUMAN	Q15678 homo sapien
16	51.5	57.2	1189	1 PTNE_MOUSE	Q62130 mus musculus
17	51	56.7	15	1 MK1_PALPR	P80408 palomona pr
18	51	56.7	180	1 XG_HUMAN	P55808 homo sapien
19	50.5	56.1	393	1 CIW4_HUMAN	Q9nyv8 homo sapien
20	50.5	56.1	1095	1 AT17_HUMAN	O8t556 homo sapien
21	50	55.6	17	1 APID_BOMPA	P81464 bombus pasc
22	50	55.6	415	1 ACRO_PIG	P08001 sus scrofa
23	50	55.6	424	1 S3B4_HUMAN	Q15427 homo sapien
24	50	55.6	449	1 ABPP_BRANA	P40803 brassica na
25	50	55.6	678	1 ABPP_RIPCL	Q27905 riptortus c
26	49	54.4	134	1 PRL5_HUMAN	Q99954 homo sapien
27	49	54.4	296	1 GDA6_WHEAT	P04726 triticum ae
28	49	54.4	352	1 RRS1_ARATH	Q9sh88 arabidopsis
29	49	54.4	2911	1 FBW2_HUMAN	P35556 homo sapien
30	48.5	53.9	2142	1 BAT2_HUMAN	P48334 homo sapien
31	48	53.3	280	1 TNF6_CERTO	Q9bnd1 cercocebus
32	48	53.3	280	1 TNF6_MACMU	Q9myl6 macaca mula
33	48	53.3	281	1 TNF6_HUMAN	P48023 homo sapien

ALIGNMENTS

RESULT 1

PR39_PIG
ID PR39_PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84; DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antibacterial protein PR-39 precursor.
GN PR39.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95350216; PubMed=7624374;
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
RT cathelin gene family member: comparative mapping of the locus for the
RT human peptide antibiotic PAL-39.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=94071853; PubMed=8250863;
RA Storici P., Zanetti M.;
RT "A cDNA derived from pig bone marrow cells predicts a sequence
RT identical to the intestinal antibacterial peptide PR-39.";
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39.";
RL FEBS Lett. 376:130-134(1995).
RN [4]
RP SEQUENCE OF 131-169.
RC TISSUE=Intestine;
RX MEDLINE=92111534; PubMed=1765098;
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Mutt V., Joernvall H.;
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new
RT member of the family of proline-arginine-rich antibacterial
RT peptides.";
RL Eur. J. Biochem. 202:849-854(1991).
RN [5]
RP SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophils;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha P.;
RT "Identification of a proline-arginine-rich antibacterial peptide from
RT neutrophils that is analogous to PR-39, an antibacterial peptide from
RT the small intestine.";

34 48 53.3 282 1 TNF6_PIG
35 48 53.3 402 1 VGLD_PRR1
36 48 53.3 520 1 C84A_ARATH
37 48 53.3 759 1 TOP3_CAEEL
38 47.5 52.8 283 1 EXTN_SORBI
39 47.5 52.8 372 1 DBPA_HUMAN
40 47.5 52.8 1443 1 SYJ2_HUMAN
41 47 52.2 147 1 SMR1_MOUSE
42 47 52.2 176 1 BCT5_BOVIN
43 47 52.2 261 1 PRP2_MOUSE
44 47 52.2 296 1 PRP3_MOUSE
45 47 52.2 507 1 MEPA_HUMAN

Q9bea8 sus scrofa
P07645 pseudorabies
Q42600 arabidopsis
O61660 caenorhabdi
P24152 sorghum bic
P16989 homo sapien
O15056 homo sapien
Q61900 mus musculus
P19660 bos taurus
P05142 mus musculus
P05143 mus musculus
Q02078 homo sapien

J. Leukoc. Biol. 56:807-811(1994).
CC -!- FUNCTION: EXERTS A POTENT ANTIMICROBIAL ACTIVITY AGAINST BOTH
CC E. COLI AND B. MEGATERIUM.
CC -!- TISSUE SPECIFICITY: SMALL INTESTINE AND BONE MARROW.
CC -!- SIMILARITY: BELONGS TO THE CATHHELICIDIN FAMILY.
CC -----
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CC EMBL; X87236; CAA60682.1; -
CC EMBL; L23825; AAA31109.1; -
CC EMBL; X89201; CAA61487.1; -
CC PIR; S68232; S68232.
CC InterPro: IPR001394; Cathelicidin.
CC Pfam: PF00666; Cathelicidins; 1.
CC ProDom: PD001838; Cathelicidins; 1.
CC ProSITE; PS00946; CATHHELICIDINS_1; 1.
CC ProSITE; PS00947; CATHHELICIDINS_2; 1.
CC KMW Antibiotic; Amidation; Signal; Pyrrolidone carboxylic acid.
CC FT SIGNAL 1 29
CC FT PROPEP 30 130
CC FT MOD_RES 131 169
CC FT CHAIN 30 30
CC FT MOD_RES 30 30
CC FT DISULFID 85 96
CC FT MOD_RES 107 124
CC FT CONFLICT 159 169
CC FT CONFLICT 21 21
CC FT CONFLICT 29 29
CC FT CONFLICT 90 91
CC FT CONFLICT 117 119
CC FT CONFLICT 157 157
CC FT CONFLICT 172 AA; 19476 MW; 994B792798C0E133 CRC64;
CC SEQUENCE 172 AA; 19476 MW; 994B792798C0E133 CRC64;
Query Match 100.0%; Score 90; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RRRPRPPYLPRLPRP 15
DB 131 RRRPRPPYLPRLPRP 145
RESULT 2
BCT7 BOVIN STANDARD; PRT; 190 AA.
AC P196L1;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bactenein 7 precursor (BAC7) (PR-59).
GN BAC7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95010707; PubMed=7925973;
RA Scocchi M., Romeo D., Zanetti M.;
RT "Molecular cloning of Bact7, a proline- and arginine-rich
RT antimicrobial peptide from bovine neutrophils.";
RL FEBS Lett. 352:197-200(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;

RA Scocchi M., Wang S., Zanetti M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 131-189.
RC TISSUE=Neutrophils;
RX MEDLINE=91035404; PubMed=2229048;
RT "Amino acid sequences of two proline-rich bactericins. Antimicrobial
RT peptides of bovine neutrophils.";
RL J. Biol. Chem. 265:18871-18874(1990).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=96300243; PubMed=8706679;
RT Storici P., Tossi A., Lenarcic B., Romeo D.;
RT "Purification and structural characterization of bovine
RT cathelicidins, precursors of antimicrobial peptides.";
RL Eur. J. Biochem. 238:769-776(1996).
CC -!- FUNCTION: EXERTS IN VITRO, A POTENT ANTIMICROBIAL ACTIVITY.
CC PROBABLY DUE TO AN IMPAIRMENT OF THE FUNCTION OF THE RESPIRATORY
CC CHAIN AND OF ENERGY-DEPENDENT ACTIVITIES IN THE INNER MEMBRANE
CC OF SUSCEPTIBLE MICROORGANISMS.
CC -!- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.
CC -!- PTM: ELASTASE IS RESPONSIBLE FOR ITS MATURATION.
CC -!- MASS SPECTROMETRY: MW=18395; MW_ERR=1; METHOD=Electrospray;
CC RANGE=30-190.
CC -!- SIMILARITY: BELONGS TO THE CATHHELICIDIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L42977; AAA87359.1; -
CC EMBL; Y09471; CAA70616.1; -
CC InterPro: IPR001894; Cathelicidin.
CC Pfam: PF00666; Cathelicidins; 1.
CC ProDom: PD001838; Cathelicidins; 1.
CC ProSITE; PS00946; CATHHELICIDINS_1; 1.
CC ProSITE; PS00947; CATHHELICIDINS_2; 1.
CC KMW Antibiotic; Repeat; Signal; Pyrrolidone carboxylic acid.
CC FT SIGNAL 1 29
CC FT PROPEP 30 130
CC FT CHAIN 131 190
CC FT PROPEP 189 190
CC FT MOD_RES 30 30
CC FT DISULFID 85 96
CC FT DISULFID 107 124
CC SEQUENCE 190 AA; 21567 MW; 8CD07D7AA30A731C CRC64;
Query Match 73.3%; Score 66; DB 1; Length 190;
Best Local Similarity 85.7%; Pred. No. 0.19;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 RRRPRPPYLPRLPRP 14
DB 132 RRRPRPPYLPRLPRP 145
RESULT 3
COTT_BACSU STANDARD; PRT; 107 AA.
ID COTT_BACSU
AC F11863;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Spore coat protein T precursor.
GN COTT.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168 / JH642;
RX  MEDLINE=9313296; PubMed=2546006;
RA  Aronson A.I., Song H.Y., Bourne N.;
RT  "Gene structure and precursor processing of a novel Bacillus subtilis
RL  spore coat protein.";
RL  Mol. Microbiol. 3:437-444(1989).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=168;
RX  MEDLINE=98044033; PubMed=9384377;
RA  Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA  Azevedo V., Bertero M.G., Bessières P., Bolotin A., Borchert S.,
RA  Borriess R., Boursier L., Brans A., Braun M., Brignelli S.C., Bron S.,
RA  Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA  Choi S.K., Codani J.J., Conneron I.P., Cummings N.J., Daniel R.A.,
RA  Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA  Entlian K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
RA  Fricz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA  Chim S.Y., Glaser P., Goffeau A., Gollighly E.J., Grandi G.,
RA  Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA  Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA  Joris B., Karimata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA  Kobayashi Y., Koeter P., Koningsstein G., Krogh S., Kumano M.,
RA  Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA  Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA  Medina N., Meliadi R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA  Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA  Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA  Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA  Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA  Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA  Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Solido B.,
RA  Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA  Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA  Tostato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA  Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA  Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA  Yoshida K., Yoshikawa H.F., Zumein E., Yoshikawa H., Danchin A.,
RT  "The complete genome sequence of the Gram-positive bacterium Bacillus
RT  subtilis.";
RL  Nature 390:249-256(1997).
CC  -!- FUNCTION: POSSIBLY PROTECTION OF SPORE AND PROBABLY PLAYS
CC  SOME ROLE IN GERMINATION.
CC  -!- SUBCELLULAR LOCATION: OUTER SURFACE OF ENDOSPORE.
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X13740; CAAJ2004.1; -
DR  EMBL; Z99110; CABJ3066.1; -
DR  PIR; S04835; A41051.
DR  Subtilist; BG10495; cotT.
KW  Sporulation; Signal; Complete proteome.
FT  SIGNAL 1 44
FT  CHAIN 45 107 SPORE COAT PROTEIN T.
SQ  SEQUENCE 107 AA; 12992 MW; AD1F66F0C4CE29A3 CRC64;
Query Match 66.1%; Score 59.5; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.6;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 4 PRPP-YLPRPRPP 15
DB 74 PRPPYYPRPP 86

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RESULT 4
BCT7 SHEEP STANDARD; PRT; 190 AA.
ID BCT7 SHEEP STANDARD; PRT; 190 AA.
AC P50415;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bactescin 7 precursor (BAC7).
GN BAC7.5.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_taxonomy:9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96105386; PubMed=7498547;
RA Bagella L., Scocchi M., Zanetti M.;
RT "cDNA sequences of three sheep myeloid cathelicidins.";
RL FEBS Lett. 376:225-228(1995).
CC -!- FUNCTION: EXERTS, IN VITRO, A POTENT ANTIMICROBIAL ACTIVITY.
CC PROBABLY DUE TO AN IMPAIRMENT OF THE FUNCTION OF THE RESPIRATORY
CC CHAIN AND OF ENERGY-DEPENDENT ACTIVITIES IN THE INNER MEMBRANE
CC OF SUSCEPTIBLE MICROORGANISMS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
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CC  -----
DR  EMBL; L46852; AAA85468.1; -
DR  PIR; S68230; S68230.
DR  InterPro; IPR001894; Cathelicidin.
DR  Pfam; PF06666; Cathelicidins; 1.
DR  ProDom; PD001838; Cathelicidin; 1.
DR  PROSITE; PS00946; CATHELICIDINS_1; 1.
DR  PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antibiotic; Repeat; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 130 BY SIMILARITY.
FT CHAIN 131 190 BACTENECIN 7.
FT MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID
FT DISULFID 85 96 (BY SIMILARITY).
FT DISULFID 107 124 BY SIMILARITY.
SQ SEQUENCE 190 AA; 21829 MW; E4A4FB1600E98371 CRC64;
Query Match 64.4%; Score 59; DB 1; Length 190;
Best Local Similarity 78.6%; Pred. No. 1.6;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 RRRPRPPYLPRPP 14
DB 132 RLPRPRPRPP 145

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RESULT 5
AP14 APINE STANDARD; PRT; 168 AA.
ID AP14 APINE STANDARD; PRT; 168 AA.
AC Q06601; P11525; P11526; P11527;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apidaecin precursor, type 14.
GN APID14.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;

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CC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93223697; PubMed=8467807;
RA Casteels-Josson K., Capaci T., Casteels P., Tempst P.;
RT "Apidaecin multipetide precursor structure: a putative mechanism for
RT amplification of the insect antibacterial response.";
RL EMBO J. 12:1569-1578 (1993).
RN [2]
RP SEQUENCE OF APIDAEACIN 1A/1B/II.
RC TISSUE=Hemolymph;
RX MEDLINE=90005446; PubMed=2676519;
RA Casteels P., Ampe C., Jacobs F., Vaecq M., Tempst P.;
RT "Apidaecins: antibacterial peptides from honeybees.";
RL EMBO J. 8:2387-2391 (1989).
CC -!- FUNCTION: APIDAEACIN HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY
CC AGAINST GRAM-NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL
CC PROPAGATION.
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CC -----
DR EMBL; X72575; CAB51167.1; -
DR PIR; S35330; S35330.
DR InterPro; IPR004828; Apidaecin.
DR Pfam; PF00807; Apidaecin; 5.
KW Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
KW Cleavage on pair of basic residues; Repeat.
FT SIGNAL 1 19
FT PROPEP 20 42
FT PEPTIDE 43 60
FT PROPEP 63 70
FT PEPTIDE 71 88
FT PROPEP 91 98
FT PROPEP 99 116
FT PROPEP 119 124
FT PEPTIDE 125 142
FT PROPEP 145 150
FT PEPTIDE 151 168
FT PEPTIDE 168 AA; 19380 MW; 5948931254C04A37 CRC64;
SQ SEQUENCE 168 AA; 19380 MW; 5948931254C04A37 CRC64;
Query Match 62.8%; Score 56.5; DB 1; Length 168;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 11; Conservative 2; Mismatches 2; Indels 7; Gaps 1;
OY 1 RRRP-----RPPVLPVPRPP 15
DB 117 REPEAEAGNRRPVIPQPRPP 138
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10] [11] [12] [13] [14] [15] [16] [17] [18] [19] [20] [21] [22] [23] [24] [25] [26] [27] [28] [29] [30] [31] [32] [33] [34] [35] [36] [37] [38] [39] [40] [41] [42] [43] [44] [45] [46] [47] [48] [49] [50] [51] [52] [53] [54] [55] [56] [57] [58] [59] [60] [61] [62] [63] [64] [65] [66] [67] [68] [69] [70] [71] [72] [73] [74] [75] [76] [77] [78] [79] [80] [81] [82] [83] [84] [85] [86] [87] [88] [89] [90] [91] [92] [93] [94] [95] [96] [97] [98] [99] [100] [101] [102] [103] [104] [105] [106] [107] [108] [109] [110] [111] [112] [113] [114] [115] [116] [117] [118] [119] [120] [121] [122] [123] [124] [125] [126] [127] [128] [129] [130] [131] [132] [133] [134] [135] [136] [137] [138] [139] [140] [141] [142] [143] [144] [145] [146] [147] [148] [149] [150] [151] [152] [153] [154] [155] [156] [157] [158] [159] [160] [161] [162] [163] [164] [165] [166] [167] [168]
RESULT 6
RNB_HSV2H
ID RNB_HSV2H STANDARD; PRT; 151 AA.
AC P89479;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Potential RNA-binding protein.
GN US11.
OS Herpes simplex virus (type 2 / strain HG52).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10315;
RN [1]
RP SEQUENCE FROM N.A.
RA Dolan A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
-----
CC -!- FUNCTION: BINDS DNA AND RNA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -----
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CC -----
DR EMBL; Z86099; CAB06719.1; -
DR DNA-binding; RNA-binding; Repeat; Nuclear protein.
FT DOMAIN 90 146
FT REPEAT 90 95
FT REPEAT 96 101
FT REPEAT 102 104
FT REPEAT 105 110
FT REPEAT 111 116
FT REPEAT 117 122
FT REPEAT 123 128
FT REPEAT 129 130
FT REPEAT 131 134
FT REPEAT 135 140
FT REPEAT 141 146
FT REPEAT 146 151
SQ SEQUENCE 151 AA; 16297 MW; FAB751F23C3DB6AE CRC64;
Query Match 61.7%; Score 55.5; DB 1; Length 151;
Best Local Similarity 73.3%; Pred. No. 2.4;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
OY 2 RRRPPVLPVPRPP 15
DB 127 RPPPPVPRPPVPRPP 141
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10] [11] [12] [13] [14] [15] [16] [17] [18] [19] [20] [21] [22] [23] [24] [25] [26] [27] [28] [29] [30] [31] [32] [33] [34] [35] [36] [37] [38] [39] [40] [41] [42] [43] [44] [45] [46] [47] [48] [49] [50] [51] [52] [53] [54] [55] [56] [57] [58] [59] [60] [61] [62] [63] [64] [65] [66] [67] [68] [69] [70] [71] [72] [73] [74] [75] [76] [77] [78] [79] [80] [81] [82] [83] [84] [85] [86] [87] [88] [89] [90] [91] [92] [93] [94] [95] [96] [97] [98] [99] [100] [101] [102] [103] [104] [105] [106] [107] [108] [109] [110] [111] [112] [113] [114] [115] [116] [117] [118] [119] [120] [121] [122] [123] [124] [125] [126] [127] [128] [129] [130] [131] [132] [133] [134] [135] [136] [137] [138] [139] [140] [141] [142] [143] [144] [145] [146] [147] [148] [149] [150] [151]
RESULT 7
T150_HUMAN
ID T150_HUMAN STANDARD; PRT; 955 AA.
AC Q9Y2W1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Thyroid hormone receptor-associated protein complex 150 kDa component
DE (Trap150).
GN TRAP150.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99214851; PubMed=10198638;
RA Ito M., Yuan C.-X., Malik S., Gu W., Pondell J.D., Yamamura S.,
RA Fu Z.-Y., Zhang X., Qin J., Roeder R.G.;
RT "Identity between TRAP and SMCC complexes indicates novel pathways for
RT the function of nuclear receptors and diverse mammalian activators.";
RL Mol. Cell 3:361-370 (1999).
RN [2]
RP SEQUENCE OF 1-672 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellanc N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Rask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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CC EMBL; X72577; CAA51169.1; --
 CC PIR; S06675; S06675.
 CC PIR; S35332; S35332.
 CC InterPro; IPR004828; Apidaecin.
 CC Pfam; PF00807; Apidaecin; 9.
 CC Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
 CC Cleavage on pair of basic residues; Repeat.
 CC NON TER 1
 CC SIGNAL <1 18 POTENTIAL.
 CC PROPEP 19 41
 CC PEPTIDE 42 59 APIDAEIN IB.
 CC PROPEP 62 69
 CC PEPTIDE 70 87 APIDAEIN IB.
 CC PROPEP 90 97
 CC PEPTIDE 98 115 APIDAEIN.
 CC PROPEP 118 125
 CC PEPTIDE 126 143 APIDAEIN IB.
 CC PROPEP 146 153
 CC PEPTIDE 154 171 APIDAEIN.
 CC PROPEP 174 182
 CC PEPTIDE 183 199 APIDAEIN IB.
 CC PROPEP 202 209
 CC PEPTIDE 210 227 APIDAEIN IB.
 CC PROPEP 230 237
 CC PEPTIDE 238 255 APIDAEIN IB.
 CC PROPEP 258 285
 CC PEPTIDE 266 283 APIDAEIN IA.
 CC SEQUENCE 283 AA; 4EA5FEDECDS142B CRC64;

Query Match 58.9%; Score 53; DB 1; Length 283;
 Best Local Similarity 72.7%; Pred. No. 8.7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPRLPRPP 15
 DB 45 REVYIPQPRPP 55

RESULT 10
 PRLP_BOVIN STANDARD; PRT; 381 AA.
 AC Q9GKN8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Prolargin precursor (Proline-arginine-rich end leucine-rich repeat protein).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP TISSUE=Articular cartilage;
 RX MEDLINE=20576219; PubMed=11007795;
 RA Bengtsson E., Aspberg A., Heinegaard D., Sommarin Y., Spillmann D.;
 RT "The amino-terminal part of PRLP binds to heparin and heparan sulfate".
 RL J. Biol. Chem. 275:40695-40702(2000).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=21964083; PubMed=11847210;
 RA Bengtsson E., Moergelin M., Sasaki T., Timpi R., Heinegaard D.,
 RA Aspberg A.;
 RT "The leucine-rich repeat protein PRLP binds perlecan and collagens and may function as a basement membrane anchor".
 RL J. Biol. Chem. 277:15061-15068(2002).

CC -!- FUNCTION: May anchor basement membranes to the underlying connective tissue.
 CC -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain.
 CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS II SUBFAMILY.
 CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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CC EMBL; AF163568; AAC23723.1; --
 CC InterPro; IPR001611; LRR.
 CC InterPro; IPR000372; LRR_Nterm.
 CC InterPro; IPR003591; LRR_Typ.
 CC Pfam; PF00560; LRR; 9.
 CC Pfam; PF01462; LRRNT; 1.
 CC PRINTS; PR00019; LEURICHREP.
 CC SMART; SM00013; LRRNT; 1.
 CC Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
 CC Signal.
 CC SIGNAL 1 21 POTENTIAL.
 CC CHAIN 22 381 PROLARGIN.
 CC DOMAIN 72 88 CIS-RICH.
 CC REPEAT 94 113 LRR-S 1.
 CC REPEAT 114 137 LRR-T 1.
 CC REPEAT 138 161 LRR-T 2.
 CC REPEAT 162 182 LRR-S 2.
 CC REPEAT 183 206 LRR-T 3.
 CC REPEAT 207 232 LRR-T 4.
 CC REPEAT 233 253 LRR-S 3.
 CC REPEAT 254 277 LRR-T 5.
 CC REPEAT 278 302 LRR-S 4.
 CC REPEAT 303 322 LRR-T 6.
 CC REPEAT 323 361 LRR-T 7.
 CC REPEAT 362 381 LRR-T 8.
 CC DOMAIN 196 201 POLY-LEU.
 CC DISULFID 331 372 BY SIMILARITY.
 CC CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 381 AA; 43682 MW; 23DA99C01BB772A0 CRC64;

Query Match 58.9%; Score 53; DB 1; Length 381;
 Best Local Similarity 76.9%; Pred. No. 12;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRPRLPRLPRPP 14
 DB 25 RRPRLPRLPRPP 37

RESULT 11
 RL1_HSV2H STANDARD; PRT; 261 AA.
 ID RL1_HSV2H
 AC P26283;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Neurovirulence factor (ICP34.5).
 GN RL1.
 OS Herpes simplex virus (type 2 / strain HG52).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;


```

CC Alphaherpesvirinae; Simplexvirus.
CC NCBI_TaxID=10315;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=92113549; PubMed=1662697;
CC McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
CC "Comparative sequence analysis of the long repeat regions and
CC adjoining parts of the long unique regions in the genomes of herpes
CC simplex viruses types 1 and 2.";
CC J. Gen. Virol. 72:3057-3075(1991).
CC [2]
CC SEQUENCE FROM N.A.
CC Dolan A.;
CC Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; D10471; BAA23428.1; -
CC EMBL; 286099; CAB06759.1; -
CC EMBL; 286099; CAB06706.1; -
CC PIR; JQ1502; WBEEXE.
CC Repeat.
CC FT DOMAIN 3 12 2 X 5 AA TANDEM REPEATS OF R-R-R-G-P.
CC FT REPEAT 3 7
CC FT REPEAT 8 12
CC FT DOMAIN 16 31 2 X 8 AA TANDEM REPEATS OF P-R-P-G-A-P-A-
CC FT REPEAT 16 23 V.
CC FT REPEAT 24 31
CC FT SEQUENCE 261 AA; 27908 MW; 4BBD13AF3D906D71 CRC64;
CC -----
CC Query Match 57.8%; Score 52; DB 1; Length 261;
CC Best Local Similarity 64.7%; Pred. No. 10;
CC Matches 11; Conservative 1; Mismatches 3; Indels 2; Gaps 1;
CC
CC QY 1 RRRPRP--EVLPRPRPP 15
CC DB 13 RRRPRGAPAVPRPGAP 29
CC
CC RESULT 12
CC ATH1_HUMAN STANDARD; PRT; 354 AA.
CC AC Q92858;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC DE Atonal protein homolog 1 (Helix-loop-helix protein HATH-1).
CC GN ATOH1 OR ATH1.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=97026280; PubMed=8872459;
CC Ben-Arie N., McCall A.B., Berkman S., Eichele G., Bellen H.J.,
CC Zoghbi H.Y.;
CC "Evolutionary conservation of sequence and expression of the bHLH
CC protein Atonal suggests a conserved role in neurogenesis.";
CC Hum. Mol. Genet. 5:1207-1216(1996).
CC CC -1- FUNCTION: ACTIVATES E BOX-DEPENDENT TRANSCRIPTION IN COLLABORATION
CC WITH E47, BUT THE ACTIVITY IS COMPLETELY ANTAGONIZED BY THE
CC NEGATIVE REGULATOR OF NEUROGENESIS HES-1. MAY PLAY A ROLE IN THE
CC DIFFERENTIATION OF SUBSETS OF NEURAL CELLS BY ACTIVATING E BOX-
CC DEPENDENT TRANSCRIPTION (BY SIMILARITY).
CC CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another

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CC BHLH protein.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC -----
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CC -----
CC EMBL; U61148; AAB41305.1; -
CC TRANSFAC; T04544; -
CC Genew; HGNC:797; ATOH1.
CC MIM; 601461; -
CC GO; GO:0003700; P:transcription factor activity; TAS.
CC GO; GO:0007417; P:central nervous system development; TAS.
CC GO; GO:0006366; P:transcription from Pol II promoter; TAS.
CC InterPro; IPR001092; HLH_basic.
CC Pfam; PF00010; HLH; 1.
CC SMART; SM00353; HLH; 1.
CC PROSITE; PS00038; HLH 1; FALSE_NEG.
CC PROSITE; PS00888; HLH 2; 1.
CC KW Transcription regulation; Activator; DNA-binding; Nuclear protein.
CC FT DOMAIN 29 38 POLY-PRO.
CC FT DNA_BIND 160 171 BASIC DOMAIN
CC FT DOMAIN 172 212 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
CC FT DOMAIN 224 228 POLY-PRO.
CC FT SEQUENCE 354 AA; 38160 MW; AB12F1E917A00A8D CRC64;
CC -----
CC Query Match 57.8%; Score 52; DB 1; Length 354;
CC Best Local Similarity 57.1%; Pred. No. 14;
CC Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 2 RRRPRPPLPRPRPP 15
CC DB 21 RRRPRPPLPRPRPP 34
CC
CC RESULT 13
CC AFCL_ARATH STANDARD; PRT; 467 AA.
CC AC P51566; Q39184;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Protein kinase AFCL (EC 2.7.1.-).
CC GN AFCL OR AME2 OR AY3G53570 OR F4P12_270.
CC OS Arabidopsis thaliana (Mouse-ear cress).
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC OC eurosids II; Brassicales; Brassicaceae; Arabidopsid.
CC OX NCBI_TaxID=3702;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. Landsberg erecta;
CC MEDLINE=95083650; PubMed=7991592;
CC Bender J., Fink G.R.;
CC "AFCL, a LAMMER kinase from Arabidopsis thaliana, activates STE12-
CC dependent processes in yeast.";
CC Proc. Natl. Acad. Sci. U.S.A. 91:12105-12109(1994).
CC [2]
CC SEQUENCE FROM N.A.
CC Kurokawa T., Yamamoto M.;
CC "A.thaliana genes encoding protein kinases of a new family.";
CC Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC [3]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. Columbia;
CC MEDLINE=21016720; PubMed=11130713;
CC Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

```

RA Partmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delsen M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choins N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weisenbach J., Saurin W., Quetier F.,
RA Schaefer M., Muelier-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordieck G.,
RA Reichelt J., Schaefer M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Otterwaelder B., Duchemin D.,
RA Cooke R., Landie M., Berger-Llauro C., Purnelle B., Masny D.,
RA De Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T.H., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RA thaliana".
RT Nature 408:820-822(2000).
RL Nature 408:820-822(2000).
CC -!- FUNCTION: ACTIVATOR OF YEAST TRANSCRIPTION FACTOR, STE12.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC LAMMER SUBFAMILY.
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CC
CC EMBL: U16176; AAA57117.1; -
CC EMBL: D45354; BAA08215.1; -
CC EMBL: AL132966; CAB67664.1; -
CC PIR: S71169; S71169.
CC HSP: P24941; IAO1.
CC InterPro: IPR000719; Prot Kinase.
CC InterPro: IPR002290; Ser_Thr_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Prot Kinase; 1.
CC SMART: SM00220; S_TK; 1.
CC SMART: SM00219; Tyrc; 1.
CC PROSITE: PS00107; PROTEIN KINASE ATP; FALSE_NEG.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC Transferrase, Serine/threonine-protein kinase; ATP-binding.
CC DOMAIN 115 443 PROTEIN KINASE.
CC FT BIND 121 129 ATP (BY SIMILARITY).
CC FT BINDING 144 144 ATP (BY SIMILARITY).
CC FT ACT SITE 240 240 BY SIMILARITY.
CC FT CONFLICT 117 117 I -> M [IN REF. 1].
CC SEQUENCE 467 AA; 54138 MW; A885FD32CE11B181 CRC64;
Query Match 57.8%; Score 52; DB 1; Length 467;
Best Local Similarity 52.4%; Pred. NO. 18;
Matches 11; Conservative 1; Mismatches 3; Indels 6; Gaps 1;
QY 1 RRRPR-----PPVLPRLPP 15
DB 35 RRRRLTWDAAAPLPPPPPP 55
RESULT 14

RELAT STRAT
ID RELAT STRAT STANDARD; PRT; 841 AA.
AC 085709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE GTP pyrophosphokinase (EC 2.7.6.5) (ATP:GTP 3'-pyrophosphotransferase)
DE (ppGpp synthetase I) ((P)ppGpp synthetase).
GN RELAT.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1890;
RX SEQUENCE FROM N.A.
RC STRAIN=IFRU 3720;
RA MEDLINE=99296594; PubMed=10368159;
RA Hoyt S., Jones G.H.;
RA "relA is required for actinomycin production in Streptomyces
RA antibioticus".
RT J. Bacteriol. 181:3824-3829(1999).
RL J. Bacteriol. 181:3824-3829(1999).
CC -!- FUNCTION: In eubacteria ppGpp (guanosine 3'-diphosphate 5'-
CC diphosphate) is a mediator of the stringent response that
CC coordinates a variety of cellular activities in responses to
CC changes in nutritional abundance. This enzyme catalyzes the
CC formation of ppGpp which is then hydrolyzed to form ppGpp (By
CC similarity). is required for actinomycin production.
CC -!- CATALYTIC ACTIVITY: ATP + GTP = AMP + Guanosine 3'-diphosphate 5'-
CC triphosphate.
CC -!- PATHWAY: ppGpp metabolism; first step.
CC -!- SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.
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CC
CC EMBL: AF072829; AAC26021.1; -
CC InterPro: IPR002912; ACT.
CC InterPro: IPR006674; HD.
CC InterPro: IPR003607; Met_phosphohydro.
CC InterPro: IPR004811; Spot_rela.
CC InterPro: IPR004095; TGS_dom.
CC Pfam: PF01842; ACT; 1.
CC Pfam: PF01966; HD; 1.
CC Pfam: PF04607; RelA_Spot; 1.
CC Pfam: PF02824; TGS; 1.
CC SMART: SM00471; HDC; 1.
CC TIGRFAMs: TIGR00691; spot_rela; 1.
CC Antitoxic biosynthesis; Transferase; Kinase.
CC SEQUENCE 841 AA; 93671 MW; 632A037BA4EF4C94 CRC64;
Query Match 57.8%; Score 52; DB 1; Length 841;
Best Local Similarity 60.0%; Pred. NO. 33;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 RRRPRPPYLPRLPP 15
DB 50 RPKAPPRPRPP 64
RESULT 15
PTNE HUMAN
ID PTNE HUMAN STANDARD; PRT; 1187 AA.
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase pez).

```

GN PTPN14 OR PEZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=95251727; PubMed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RA Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RT ezrin-like domains.";
RL Biochem. Biophys. Res. Commun. 209:959-965(1995).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF HUMAN TISSUES
CC INCLUDING KIDNEY, SKELETAL MUSCLE, LUNG AND PLACENTA.
CC -!- SIMILARITY: Contains 1 PFM domain.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
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CC -----
DR EMBL; X82676; CAA57993.1; .
DR PIR; JC4155; JC4155.
DR HSSP; P29350; IGWZ.
DR Genew; HGNC:9647; PTPN14.
DR MIM; 603155; .
DR GO; GO:0006470; P; protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 4.1; 1.
DR Pfam; PF00102; Y-phosphatase; 1.
DR PRINTS; PR00935; BAND4.1.
DR PRINTS; PR00700; PRTPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00660; PFM_1; 1.
DR PROSITE; PS00661; PFM_2; 1.
DR PROSITE; PS50057; PFM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW Structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM.
FT DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1121 1121 BY SIMILARITY.
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 709 716 POLY-GLU.
SQ SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;
Query Match 57.3%; Score 51.5; DB 1; Length 1187;
Best Local Similarity 81.3%; Pred. No. 52;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 3 RPPPPYLP RPP 14
DB 565 RPPPPY-P RPP 575

```

Search completed: October 1, 2003, 19:03:41
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2003, 19:00:08 ; Search time 93 seconds
(without alignments)
41.621 Million cell updates/sec

Title: US-09-426-01ld-3

Perfect score: 90

Sequence: 1 RRRPPPLPRPRPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	67.8	336	12 Q68405	Q68405 human cytom
2	58	64.4	156	10 Q8RV32	Q8RV32 oryza sativ
3	58	64.4	184	6 P79361	P79361 ovis aries
4	58	64.4	190	6 Q9XSO9	Q9XSO9 capra hircu
5	58	64.4	224	6 O19031	O19031 ovis aries
6	58	64.4	1729	10 Q8LIL20	Q8LIL20 oryza sativ
7	57.5	63.9	183	10 Q94J98	Q94J98 oryza sativ
8	57	63.3	200	16 Q9RK54	Q9RK54 streptomyc
9	57	63.3	361	2 Q9XCG4	Q9XCG4 mycobacteri
10	56	62.2	212	2 O08306	O08306 nocardioide
11	55	61.1	212	12 O41980	O41980 murid herpe
12	55	61.1	464	12 Q91TM2	Q91TM2 tupiaia herp
13	54.5	60.6	301	10 Q41848	Q41848 zea mays (m
14	54.5	60.6	2635	12 Q40942	Q40942 kaposi's sa
15	54.5	60.6	2635	12 P89955	P89955 kaposi's sa
16	54	60.0	144	10 Q8LWN3	Q8LWN3 oryza sativ

ALIGNMENTS

RESULT 1

Q68405 PRELIMINARY; PRT; 336 AA.
AC Q68405;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Orf UL151.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Toledo;
RX MEDLINE=96099416; PubMed=85233595;
RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
RT "Human cytomegalovirus clinical isolates carry at least 19 genes not
found in laboratory strains.";
RL J. Virol. 70:78-83(1996).
DR EMBL; U33331; AAA85892.1; -;
SQ SEQUENCE 336 AA; 35116 MW; 9F865B5019F69D0C CRC64;

Query Match 67.8%; Score 61; DB 12; Length 336;
Best Local Similarity 78.6%; Pred. No. 0.92; Mismatches 0; Gaps 0;
Matches 11; Conservative 0; Indels 3

QY 2 RRRPPPLPRPRPP 15

|||||
279 RRRPPPLPRPRPP 292

RESULT 2

Q8RV32 PRELIMINARY; PRT; 156 AA.
ID Q8RV32;
AC Q8RV32;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

Q8RV32 mus musculu
Q9XZT0 drosophila
Q4582 caenorhabdi
Q95X63 caenorhabdi
Q8BV76 mus musculu
Q8BZ7 mus musculu
Q99JA6 mus musculu
Q8BKT2 mus musculu
Q9SM77 oryza sativ
Q23291 caenorhabdi
Q9JFF6 oryza sativ
Q8WE93 apis mellif
Q9XIZ3 oryza sativ
Q2370 arabidopsis
Q82066 solanum tub
Q9LV14 arabidopsis
Q66852 fowl adenov
Q8U5T2 agrobacteri
Q96E55 homo sapien
Q42421 beta vulgar
Q8T458 drosophila
Q8MME1 drosophila
Q9LMQ1 arabidopsis
Q9WIZ6 drosophila
Q8V718 sinian herp
Q8W097 oryza sativ
Q8C3A1 mus musculu
Q8CE88 mus musculu
Q8CAV9 mus musculu

DE OSJNB0032K15.1 protein (QJ1159.D09.32 protein).
 GN OSJNB0032K15.1 OR QJ1159.D09.32.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 RT clone:OSJNB0032K15.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 RT clone:OJ1159.D09.32";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003710; SAB86560.1;
 DR EMBL; AP003792; SAB89214.1;
 DR Genbank; O8RV22;
 SQ SEQUENCE 156 AA; 17659 MW; 4152112C3DB493CF CRC64;

Query Match 64.4%; Score 58; DB 10; Length 156;
 Best Local Similarity 73.3%; Pred. No. 1.1;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRLPRP 15
 |||||
 DB 78 RRRPRPPYLPRLPRP 92

RESULT 3

P79361
 ID P79361 PRELIMINARY; PRT; 164 AA.
 AC P79361;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE 7.5 kDa bactinecin (Fragment).
 GN BAC7.5.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Mahoney M.M., Lee A.Y., Brzinski-Caliguri D.J., Huttner K.M.;
 RT "Molecular analysis of the sheep cathelin family reveals a novel
 RT antimicrobial peptide.";
 RL FEBS Lett. 377:519-522(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Huttner K.M., Mahoney M.M.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U60598; A849713.1;
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidins; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 FT NON_TER 164 AA; 18642 MW; E3BFC871F6AB9B9A CRC64;
 SQ SEQUENCE 164 AA; 18642 MW; E3BFC871F6AB9B9A CRC64;

Query Match 64.4%; Score 58; DB 6; Length 164;
 Best Local Similarity 78.6%; Pred. No. 1.2;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RRRPRPPYLPRLPRP 14
 |||||
 DB 132 RLRPRRLPRP 145

RESULT 4

Q9XSQ9
 ID Q9XSQ9 PRELIMINARY; PRT; 190 AA.
 AC Q9XSQ9;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE BAC7.5 protein.
 GN BAC7.5.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Zhao C., Nguyen T., Brogden K., Lehrer R.;
 RT "cDNA cloning of goat cathelin related peptides.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243125; CAB45523.1;
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidins; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 FT CHAIN 131 190 BAC7.5 PROTEIN.
 SQ SEQUENCE 190 AA; 21835 MW; D13305EF16875F4F CRC64;

Query Match 64.4%; Score 58; DB 6; Length 190;
 Best Local Similarity 78.6%; Pred. No. 1.3;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRLPRP 14
 |||||
 DB 132 RLRPRRLPRP 145

RESULT 5

O19031
 ID O19031 PRELIMINARY; PRT; 224 AA.
 AC O19031;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE BACTINECIN 11 precursor.
 GN BAC11.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
 RT "Localization and genomic organization of sheep antimicrobial peptides
 RT genes.";
 RL Gene 206:85-91(1998).
 CC -1- FUNCTION: ANTIMICROBIAL PEPTIDE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
 DR EMBL; U77049; AAB62000.1;
 DR EMBL; U77046; AAB62000.1; JOINED.
 DR EMBL; U77047; AAB62000.1; JOINED.
 DR EMBL; U77048; AAB62000.1; JOINED.
 DR InterPro; IPR001894; Cathelicidin.

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DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
DR Signal; Antibiotic.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 130 POTENTIAL.
FT CHAIN 131 224 BACTINECIN 11.
FT MOD_RES 30 30 PYROLIDONE CARBOXYLIC ACID (BY
FT DISULFID 85 96 BY SIMILARITY).
FT DISULFID 107 124 BY SIMILARITY.
SQ SEQUENCE 224 AA; 25669 MW; 6AEAAAB1256AC76FC CRC64;

Query Match 64.4%; Score 58; DB 6; Length 224;
Best Local Similarity 78.6%; Pred. No. 1.6;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPLPRPP 14
Db 132 RLPRPRPLPRPP 145

RESULT 6
Q8LLZ0 PRELIMINARY; PRT; 1729 AA.
AC Q8LLZ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative retroelement.
GN OSJNAA0028C16.15.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
RA Currie J., Collura K.;
RT "Rice Genomic Sequence."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC131966; AA04923.1; -.
DR Gramene; Q8LLZ0; -.
DR InterPro; IPR001969; Asparticase site.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RTase.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00078; rvt; 2.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS00158; ZF_CCHC; 1.
DR RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1729 AA; 197883 MW; 6FA3642FD34B4E33 CRC64;

Query Match 64.4%; Score 58; DB 10; Length 1729;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPRPPLPRPP 15
Db 71 RRRPRPPLRRRPP 85

RESULT 7
Q94J98 PRELIMINARY; PRT; 183 AA.
ID Q94J98

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AC Q94J98;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0047B08.14 protein (QJ1159 D09.5 protein).
GN P0047B08.14 OR QJ1159 D09.5.
OS Oryza sativa (Rice), and
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0047B08."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
RT clone: QJ1159 D09."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003053; BAB55690.1; -.
DR EMBL; AP003792; BAB89188.1; -.
DR Gramene; Q94J98; -.
SQ SEQUENCE 183 AA; 20155 MW; F1CF823AD89CEB36 CRC64;

Query Match 63.9%; Score 57.5; DB 10; Length 183;
Best Local Similarity 73.3%; Pred. No. 1.5;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 RRRPRPPLPRPP 15
Db 129 RSRPR-PYAPRPQP 142

RESULT 8
Q9K54 PRELIMINARY; PRT; 200 AA.
AC Q9K54;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO0323.
GN SCO0323 OR SCF12.02C
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A3(2) / M145;
RA MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939105; CAB56128.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 200 AA; 22076 MW; 0DCBEC5585803B5 CRC64;

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Query Match 53.3%; Score 57; DB 16; Length 200;
Best Local Similarity 76.9%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPR 13
DB 118 RRRPPPPYLP RPR 130

RESULT 9
Q9XCG4 PRELIMINARY; PRT; 361 AA.
AC Q9XCG4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 40.2 kDa protein.
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2151;
RA Eckstein T.M., Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.;
RT "Identification of a gene cluster involved in glycopeptidolipid
biosynthesis and of a gene cluster encoding daunorubicin resistance in
two strains of Mycobacterium avium serovar 2";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF143772; AAD44199.1;
KW Hypothetical protein.
SQ SEQUENCE 361 AA; 42028 MW; AD01DB825C1C9EA CRC64;

Query Match 63.3%; Score 57; DB 2; Length 361;
Best Local Similarity 71.4%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPR 14
DB 32 RRRPPPPYLP RPR 45

RESULT 10
O08306 PRELIMINARY; PRT; 212 AA.
AC O08306;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 23.7 kDa protein.
OS Nocardioideae simplex (Arthrobacter simplex).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacterineae; Nocardioidaceae; Pimelobacter.
OX NCBI_TaxID=2045;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO12069;
RA Molnar I., Choi K., Yamashita M., Murooka Y.;
RT "Molecular cloning, expression in Streptomyces lividans, and analysis
of a gene cluster from Arthrobacter simplex encoding 3-
ketosteroid-DELTA.1-dehydrogenase, 3-ketosteroid-DELTA.5-isomerase
and a hypothetical regulatory protein";
RL Mol. Microbiol. 15:895-905 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO12069;
RA Dziadek J., Yamashita M., Murooka Y.;
RT "Cloning, sequencing and characterization of the downstream region of
KsdDI operon of Arthrobacter simplex";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TETR/ACR FAMILY OF TRANSCRIPTIONAL
REGULATORS.

DR EMBL; Z93338; CAB07542.1;
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; tetr; 1.
DR PRINTS; PR00455; HTH_TETR.
DR PROSITE; PS01081; HTH_TETR_FAMILY; 1.
KW Hypothetical protein; DNA-Binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 212 AA; 22740 MW; F9118E18DDF4E0B2 CRC64;

Query Match 62.2%; Score 56; DB 2; Length 212;
Best Local Similarity 73.3%; Pred. No. 2.8;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPR 15
DB 83 RRRPPPPYLP RPR 97

RESULT 11
O41980 PRELIMINARY; PRT; 212 AA.
AC O41980;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Hypothetical 21.9 kDa protein.
GN GAMMAHV M13.
OS Murid herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=33708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WUMS;
RX MEDLINE=97366649; PubMed=9223479;
RA Virgin H.W. IV, Latreille P., Wamsley P., Hallsworth K., Weck K.E.,
RA Dal Canto A.J., Speck S.H.;
RT "Complete sequence and genomic analysis of murine gammaherpesvirus
68";
RL J. Virol. 71:5894-5904 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WUMS;
RA Latreille P., Wamsley P., Waterston R.H.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97553; AAB6426.1;
KW Hypothetical protein.
SQ SEQUENCE 212 AA; 21911 MW; E066860064282149 CRC64;

Query Match 61.1%; Score 55; DB 12; Length 212;
Best Local Similarity 75.0%; Pred. No. 3.8;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RRRPPPPYLP RPR 15
DB 136 RRRPPPPYLP RPR 147

RESULT 12
Q91TM2 PRELIMINARY; PRT; 464 AA.
AC Q91TM2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE T74.
OS Tupaia herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae.
OX NCBI_TaxID=10397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2;

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RX MEDLINE=21211637; PubMed=11312357;
RA Bahr U., Darai G.;
RT "Analysis and Characterization of the Complete Genome of Tupaia (Tree
RL Shrew) Herpesvirus.";
RN J. Virol. 75:4854-4870(2001).
RP SEQUENCE FROM N.A.
RC STRAIN=2;
RA Darai G., Bahr U.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF281817; AAK57119.1; -.
SQ SEQUENCE 464 AA; 51193 MW; 4BB7313EA2C2ED16 CRC64;

Query Match 61.1%; Score 55; DB 12; Length 464;
Best Local Similarity 76.9%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRPYPYLP-PPRPP 15
Db 421 RRPYPYLP-PPRPP 433

RESULT 13
Q41848 PRELIMINARY; PRT; 301 AA.
AC Q41848;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Prolin rich protein.
GN PRP.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
ON [3]
RP SEQUENCE FROM N.A.
RC STRAIN=W64A;
RX MEDLINE=92361259; PubMed=1498600;
RA Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;
RT "A maize embryo-specific gene encodes a proline-rich and hydrophobic
RL protein.";
RL Plant Cell 4:413-423(1992).
DR EMBL; X60432; CAA42959.1; -.
DR HSPF; P24337; LHYP.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR002965; P rich extensn.
DR Pfam; PF00234; trypt alpha amyl. 1.
DR PRINTS; PR01217; PRICHEXTENSN.
DR SMART; SM00499; AAI.1
SQ SEQUENCE 301 AA; 31647 MW; 884EB70854D28C2E CRC64;

Query Match 60.6%; Score 54.5; DB 10; Length 301;
Best Local Similarity 71.4%; Pred. No. 6.1;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 3 RRPYPYLP-PPRPP 15
Db 149 RRPYPYLP-PPRPP 162

RESULT 14
O40942 PRELIMINARY; PRT; 2635 AA.
AC O40942;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ORF 64.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.

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OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296220; PubMed=9151804;
RA Neipel F., Albrecht J.C., Fleckenstein B.;
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RL human herpesvirus 8: determinants of its pathogenicity?";
RN J. Virol. 71:4187-4192(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RT "The genome of human herpesvirus 8 cloned from Kaposi's sarcoma.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93872; AAB62600.1; -.
DR InterPro; IPR006928; Herpes teg N.
DR InterPro; IPR002965; P rich extensn.
DR Pfam; PF04843; Herpes teg N; 1.
DR PRINTS; PR01217; PRICHEXTENSN.
SQ SEQUENCE 2635 AA; 289717 MW; 91DDA0D6FF7B660A CRC64;

Query Match 60.6%; Score 54.5; DB 12; Length 2635;
Best Local Similarity 68.4%; Pred. No. 48;
Matches 13; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

Qy 2 RRPYPYLP-PPRPP 15
Db 271 RRPYPYLP-PPRPP 289

RESULT 15
P88955 PRELIMINARY; PRT; 2635 AA.
AC P88955;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ORF 64.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
ON [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871;
RA Moore P.S., Boshoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RL genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121480; PubMed=8962146;
RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RL (SHV8).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75698; AAC57149.1; -.
DR InterPro; IPR006928; Herpes teg N.
DR InterPro; IPR002965; P rich extensn.
DR Pfam; PF04843; Herpes teg N; 1.
DR PRINTS; PR01217; PRICHEXTENSN.
SQ SEQUENCE 2635 AA; 289667 MW; 00070132EA8139AF CRC64;

Query Match 60.6%; Score 54.5; DB 12; Length 2635;
Best Local Similarity 68.4%; Pred. No. 48;
Matches 13; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

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Oy 2 RRRP---PPVLP--RRPP 15
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Db 271 RRPVVIPPYD&TDRPP 289

Search completed: October 1, 2003, 19:05:23
Job time : 95 secs